

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 6, 2004, 12:41:36 ; Search time 39 Seconds  
(without alignment)  
186.075 Million cell updates/sec

Title: US-10-612-885A-1  
Perfect score: 117  
Sequence: 1 QRVLEIGRTECVLSNLRGTRY 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_25.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	109	93.2	316	11	O35545
2	107	91.5	509	6	Q9MYZ9
3	104	88.9	229	6	Q28206
4	104	88.9	229	6	Q27950
5	104	88.9	387	6	Q95N13
6	104	88.9	418	6	Q95N14
7	56	47.9	176	17	Q8TYF5
8	52	44.4	1028	4	Q9UQ52
9	49	41.9	836	2	Q9AXX8
10	49	41.9	1028	11	P97528
11	48	41.0	428	10	Q9LPY7
12	48	41.0	1028	11	Q9JMB8
13	48	41.0	1028	11	Q8G6X1
14	47	40.2	539	10	Q94LS6
15	47	40.2	539	10	Q7XDN4
16	47	40.2	640	10	Q9ASX3

17	47	40.2	644	10	Q8LDV1
18	47	40.2	644	10	Q9FNK3
19	47	40.2	1226	16	Q7UL12
20	47	40.2	1873	10	Q9FG11
21	46	39.3	288	12	Q98214
22	46	39.3	637	5	Q86GJ9
23	46	39.3	700	11	Q9CXF5
24	46	39.3	700	11	Q8COB3
25	46	39.3	781	15	Q83857
26	46	39.3	1283	5	Q8TA82
27	45.5	38.9	95	3	Q8TF83
28	45	38.5	76	7	Q30734
29	45	38.5	76	7	Q30567
30	45	38.5	81	7	Q30747
31	45	38.5	316	16	Q912J3
32	45	38.5	446	10	Q94CT7
33	45	38.5	479	5	Q9U7P5
34	45	38.5	567	5	Q95R48
35	45	38.5	567	5	Q9VCA3
36	45	38.5	773	16	Q8AOC0
37	45	38.5	968	5	Q7Y247
38	45	38.5	1056	12	O57161
39	44.5	38.0	691	5	Q9VML1
40	44.5	38.0	693	5	Q96680
41	44.5	38.0	810	10	Q92W13
42	44	37.6	47	16	Q8XFL2
43	44	37.6	195	16	Q8ZOG3
44	44	37.6	606	5	Q9VWF6
45	44	37.6	2023	12	O91632

## ALIGNMENTS

### RESULT 1

O35545 PRELIMINARY; PRT; 316 AA.  
ID AC O35545 (T-EMBLrel. 05, Created)  
DT 01-JAN-1998 (T-EMBLrel. 05, Last sequence update)  
DT 01-JAN-1998 (T-EMBLrel. 25, Last annotation update)  
DE Intron 5-inserted form of erythropoietin receptor precursor.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98296111; PubMed=9630610;  
RA Yamaji R., Murakami C., Takenoshita M., Tsuyama S., Inui H.,  
RA Miyatake K., Nakano Y.,  
RT "The intron 5-inserted form of rat erythropoietin receptor is expressed as a membrane-bound form."  
RL Biochim. Biophys. Acta 1403:169-178(1998).  
DR EMBL; D83509; BAA22373.1; -  
DR HSSP; P19235; 1EBA.  
DR GO; GO:0016020; C-membrane; IEA.  
DR GO; GO:0004892; F-hematopoietin/interferon-class (D200-domain. . .; IEA.  
DR GO; GO:0004892; F-receptor activity; IEA.  
DR InterPro; IPR002996; CR1A.  
DR InterPro; IPR003961; FN III.  
DR InterPro; IPR008957; FN\_III-like.  
DR InterPro; IPR003528; Hemopoetn\_L\_F1.  
DR Pfam; PF00041; fn3; 1.  
DR SMART; SM00060; FN3; 1.  
DR PROSITE; PS01352; HEMATOPO\_REC\_L\_F1; 1.  
KW Receptor; Signal.  
FT SIGNAL 1 24 POTENTIAL.  
FT CHAIN 25 316 POTENTIAL.  
SQ SEQUENCE 316 AA; 34220 MW; 05C44BF8516C180B CRC64;

Query Match 93.2%; Score 109; DB 11; Length 316;  
Best Local Similarity 91.3%; Pred. No. 6.8e-10;

Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QRVLEGRTECVLSNLRGTRY 23  
DB 193 QRVLEGRTECVLSNLRGTRY 215

RESULT 2  
Q9MYZ9 PRELIMINARY; PRT; 509 AA.

AC Q9MYZ9 (TREMELrel. 15, Created)  
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)  
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
DE Erythropoietin receptor.  
OS Sus scrofa (pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RA Pearson P.L.; Smith T.P.L.; Sonstegard T.S.; Klemcke H.G.;  
RA Christensen R.K.; Vallier J.L.;  
RT "Porcine Erythropoietin Receptor: Molecular Cloning and Expression in  
RT Embryonic and Fetal Liver."  
RL Domest. Anim. Endocrinol. 0:0-0(2000).  
DR EMBL; AF274305; AAF77065.1; -.  
DR HSSP; P19235; IEBA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0006118; P:electron transport; IEA.  
DR InterPro; IPR002996; CR1A.  
DR InterPro; IPR003961; FN III.  
DR InterPro; IPR008957; FN III-like.  
DR InterPro; IPR003528; Hemopoetn\_L\_Fl.  
DR Pfam; PF00041; fn3; 1.  
DR SMART; SM00060; FN3; 1.  
DR PROSITE; PS01352; HEMATOPO\_REC\_L\_F1; 1.  
KW Receptor.  
SQ SEQUENCE 509 AA; 55183 MW; 35B565D07C6BCD8A CRC64;

Query Match 91.5%; Score 107; DB 6; Length 509;  
Best Local Similarity 91.3%; Pred. No. 2.5e-09;  
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QRVLEGRTECVLSNLRGTRY 23  
DB 195 QRVLEGRTECVLSNLRGTRY 217

RESULT 3  
Q28206 PRELIMINARY; PRT; 229 AA.

AC Q28206 (TREMELrel. 01, Created)  
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
DE Erythropoietin receptor (fragment).  
GN EPOR.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Bone marrow;  
RA Suliman H.B.; Feldman B.F.; Majiwa P.A.O.; Logan-Henfrey L.L.;  
RA Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

Query Match 91.3%; Score 107; DB 6; Length 509;  
Best Local Similarity 91.3%; Pred. No. 2.5e-09;  
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QRVLEGRTECVLSNLRGTRY 23  
DB 195 QRVLEGRTECVLSNLRGTRY 217

RESULT 3  
Q28206 PRELIMINARY; PRT; 229 AA.

AC Q28206 (TREMELrel. 01, Created)  
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
DE Erythropoietin receptor (fragment).  
GN EPOR.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Bone marrow;  
RA Suliman H.B.; Feldman B.F.; Majiwa P.A.O.; Logan-Henfrey L.L.;  
RA Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

Query Match 91.3%; Score 107; DB 6; Length 509;  
Best Local Similarity 91.3%; Pred. No. 2.5e-09;  
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QRVLEGRTECVLSNLRGTRY 23  
DB 195 QRVLEGRTECVLSNLRGTRY 217

RESULT 3  
Q28206 PRELIMINARY; PRT; 229 AA.

AC Q28206 (TREMELrel. 01, Created)  
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
DE Erythropoietin receptor (fragment).  
GN EPOR.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Bone marrow;  
RA Suliman H.B.; Feldman B.F.; Majiwa P.A.O.; Logan-Henfrey L.L.;  
RA Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U61399; AAB03871.1; -.  
DR HSSP; P19235; IEBA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR002996; CR1A.  
DR InterPro; IPR003961; FN III.  
DR InterPro; IPR008957; FN III-like.  
DR InterPro; IPR003528; Hemopoetn\_L\_Fl.  
DR Pfam; PF00041; fn3; 1.  
DR SMART; SM00060; FN3; 1.  
DR PROSITE; PS01352; HEMATOPO\_REC\_L\_F1; 1.  
KW Receptor.  
FT NON\_TER 229 229  
SQ SEQUENCE 229 AA; 25170 MW; EDFAA6F110D992E8 CRC64;

Query Match 88.9%; Score 104; DB 6; Length 229;  
Best Local Similarity 87.0%; Pred. No. 3.3e-09;  
Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QRVLEGRTECVLSNLRGTRY 23  
DB 136 QRVLEGRTECVLSNLRGTRY 158

RESULT 4  
Q27950 PRELIMINARY; PRT; 229 AA.

AC Q27950 (TREMELrel. 01, Created)  
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
DE Erythropoietin receptor (fragment).  
GN EPOR.  
OS Bos indicus (Zebu).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9915;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Bone marrow;  
RA Suliman H.B.; Feldman B.F.; Majiwa P.A.O.; Logan-Henfrey L.L.;  
RA Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

Query Match 88.9%; Score 104; DB 6; Length 229;  
Best Local Similarity 87.0%; Pred. No. 3.3e-09;  
Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QRVLEGRTECVLSNLRGTRY 23  
DB 136 QRVLEGRTECVLSNLRGTRY 158

RESULT 4  
Q27950 PRELIMINARY; PRT; 229 AA.

AC Q27950 (TREMELrel. 01, Created)  
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
DE Erythropoietin receptor (fragment).  
GN EPOR.  
OS Bos indicus (Zebu).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9915;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Bone marrow;  
RA Suliman H.B.; Feldman B.F.; Majiwa P.A.O.; Logan-Henfrey L.L.;  
RA Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

Query Match 88.9%; Score 104; DB 6; Length 229;  
Best Local Similarity 87.0%; Pred. No. 3.3e-09;  
Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QRVLEGRTECVLSNLRGTRY 23  
DB 136 QRVLEGRTECVLSNLRGTRY 158

RESULT 5  
Q95N13

Q95N13 PRELIMINARY; PRT; 387 AA.  
AC Q95N13;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Erythropoietin receptor (Fragment).  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA David B., Lim G.B., Moritz K.M., Koukoulas I., Wintour M.;  
RT "Quantitation of the mRNA levels of Epo and Epor in various tissues in  
the ovine fetus."  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR ENBL; AY029232; AAK38737.1; -  
DR GO; GO:0016020; C-membrane; IEA.  
DR GO; GO:0004896; F-hematopoietin/interferon-class (D200-domain. . . ; IEA.  
DR GO; GO:0004872; F-receptor activity; IEA.  
DR InterPro; IPR003961; FN III.  
DR InterPro; IPR008957; FN\_III-like.  
DR InterPro; IPR003528; Hemopoetn\_L\_F1.  
DR Pfam; PF00041; fn3; 1.  
DR SMART; SM00060; FN3; 1.  
DR PROSITE; PS01352; HEMATOPO\_REC\_L\_F1; 1.  
KW Receptor.  
FT NON\_TER  
FT NON\_TER  
SQ SEQUENCE 387 AA; 42039 MW; 0D1E6173C432EBC6 CRC64;  
Query Match 88.9%; Score 104; DB 6; Length 387;  
Best Local Similarity 87.0%; Pred. No. 5.9e-09;  
Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 QRVLEIGRTECVLSNLRGTRY 23  
Db 130 QRVLEIGRTECVLSNLRGTRY 152  
RESULT 6  
Q95N14 PRELIMINARY; PRT; 418 AA.  
AC Q95N14;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Erythropoietin receptor (Fragment).  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA David B., Lim G.B., Moritz K.M., Koukoulas I., Wintour M.;  
RT "Quantitation of the mRNA levels of Epo and Epor in various tissues in  
the ovine fetus."  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR ENBL; AY029231; AAK38170.1; -  
DR GO; GO:0016020; C-membrane; IEA.  
DR GO; GO:0004896; F-hematopoietin/interferon-class (D200-domain. . . ; IEA.  
DR GO; GO:0004872; F-receptor activity; IEA.  
DR InterPro; IPR003961; FN III.  
DR InterPro; IPR008957; FN\_III-like.  
DR Pfam; PF00041; fn3; 1.  
DR SMART; SM00060; FN3; 1.  
DR PROSITE; PS01352; HEMATOPO\_REC\_L\_F1; 1.  
KW Receptor.  
FT NON\_TER  
FT NON\_TER  
SQ SEQUENCE 418 AA; 45282 MW; BB742EBEA034503C CRC64;  
Query Match 88.9%; Score 104; DB 6; Length 418;  
Best Local Similarity 87.0%; Pred. No. 6.4e-09;  
Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 QRVLEIGRTECVLSNLRGTRY 23  
Db 130 QRVLEIGRTECVLSNLRGTRY 152  
RESULT 7  
Q8TYF5 PRELIMINARY; PRT; 176 AA.  
AC Q8TYF5;  
DT 01-JUN-2002 (TREMBlrel. 21, Created)  
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Uncharacterized protein.  
GN MK0345.  
OS Methanopyrus kandleri.  
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;  
OC Methanopyrus.  
OX NCBI\_TaxID=2320;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AV19 / DSM 6324 / JCM 9639;  
RX MEDLINE=21927647; PubMed=11930014;  
RA Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,  
RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,  
RA Matthe D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,  
RA Malykh A.G., Koonin E.V., Kozhavkin S.A.;  
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19  
and monophyly of archaeal methanogens."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649 (2002).  
DR ENBL; AS010332; AAM01560.1; -  
DR InterPro; IPR009003; Cys\_Ser\_trypsin.  
KW Complete proteome.  
SQ SEQUENCE 176 AA; 19285 MW; 81E181C7BF3BBD8B CRC64;  
Query Match 47.9%; Score 56; DB 17; Length 176;  
Best Local Similarity 52.4%; Pred. No. 0.3;  
Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
QY 2 RVEILGRTECVLSNLRGTR 22  
Db 150 RMDVIEETERALKRLRGQR 170  
RESULT 8  
Q9UQ52 PRELIMINARY; PRT; 1028 AA.  
AC Q9UQ52;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Neural adhesion molecule NB-3.  
GN HNB-3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=98146168; PubMed=9486763;  
RX Kamei Y., Tsutsumi O., Taketani Y., Watanabe K.;  
RT "cDNA cloning and chromosomal localization of neural adhesion  
molecule, NB-3 in human."  
RL J. Neurosci. Res. 51:275-283 (1998).  
DR ENBL; AB003592; BAA82612.1; -  
DR HSSP; P20241; 1CFB.  
DR Genew; HGNC:2176; CNTN6.  
DR GO; GO:0007155; P:cell adhesion; TAS.

Q95N13 PRELIMINARY; PRT; 387 AA.  
AC Q95N13;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Erythropoietin receptor (Fragment).  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA David B., Lim G.B., Moritz K.M., Koukoulas I., Wintour M.;  
RT "Quantitation of the mRNA levels of Epo and Epor in various tissues in  
the ovine fetus."  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR ENBL; AY029232; AAK38737.1; -  
DR GO; GO:0016020; C-membrane; IEA.  
DR GO; GO:0004896; F-hematopoietin/interferon-class (D200-domain. . . ; IEA.  
DR GO; GO:0004872; F-receptor activity; IEA.  
DR InterPro; IPR003961; FN III.  
DR InterPro; IPR008957; FN\_III-like.  
DR InterPro; IPR003528; Hemopoetn\_L\_F1.  
DR Pfam; PF00041; fn3; 1.  
DR SMART; SM00060; FN3; 1.  
DR PROSITE; PS01352; HEMATOPO\_REC\_L\_F1; 1.  
KW Receptor.  
FT NON\_TER  
FT NON\_TER  
SQ SEQUENCE 387 AA; 42039 MW; 0D1E6173C432EBC6 CRC64;  
Query Match 88.9%; Score 104; DB 6; Length 387;  
Best Local Similarity 87.0%; Pred. No. 5.9e-09;  
Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 QRVLEIGRTECVLSNLRGTRY 23  
Db 130 QRVLEIGRTECVLSNLRGTRY 152  
RESULT 6  
Q95N14 PRELIMINARY; PRT; 418 AA.  
AC Q95N14;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Erythropoietin receptor (Fragment).  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA David B., Lim G.B., Moritz K.M., Koukoulas I., Wintour M.;  
RT "Quantitation of the mRNA levels of Epo and Epor in various tissues in  
the ovine fetus."  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR ENBL; AY029231; AAK38170.1; -  
DR GO; GO:0016020; C-membrane; IEA.  
DR GO; GO:0004896; F-hematopoietin/interferon-class (D200-domain. . . ; IEA.  
DR GO; GO:0004872; F-receptor activity; IEA.  
DR InterPro; IPR003961; FN III.  
DR InterPro; IPR008957; FN\_III-like.  
DR Pfam; PF00041; fn3; 1.  
DR SMART; SM00060; FN3; 1.  
DR PROSITE; PS01352; HEMATOPO\_REC\_L\_F1; 1.  
KW Receptor.  
FT NON\_TER  
FT NON\_TER  
SQ SEQUENCE 418 AA; 45282 MW; BB742EBEA034503C CRC64;  
Query Match 88.9%; Score 104; DB 6; Length 418;  
Best Local Similarity 87.0%; Pred. No. 6.4e-09;  
Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 QRVLEIGRTECVLSNLRGTRY 23  
Db 130 QRVLEIGRTECVLSNLRGTRY 152  
RESULT 7  
Q8TYF5 PRELIMINARY; PRT; 176 AA.  
AC Q8TYF5;  
DT 01-JUN-2002 (TREMBlrel. 21, Created)  
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Uncharacterized protein.  
GN MK0345.  
OS Methanopyrus kandleri.  
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;  
OC Methanopyrus.  
OX NCBI\_TaxID=2320;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AV19 / DSM 6324 / JCM 9639;  
RX MEDLINE=21927647; PubMed=11930014;  
RA Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,  
RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,  
RA Matthe D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,  
RA Malykh A.G., Koonin E.V., Kozhavkin S.A.;  
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19  
and monophyly of archaeal methanogens."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649 (2002).  
DR ENBL; AS010332; AAM01560.1; -  
DR InterPro; IPR009003; Cys\_Ser\_trypsin.  
KW Complete proteome.  
SQ SEQUENCE 176 AA; 19285 MW; 81E181C7BF3BBD8B CRC64;  
Query Match 47.9%; Score 56; DB 17; Length 176;  
Best Local Similarity 52.4%; Pred. No. 0.3;  
Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
QY 2 RVEILGRTECVLSNLRGTR 22  
Db 150 RMDVIEETERALKRLRGQR 170  
RESULT 8  
Q9UQ52 PRELIMINARY; PRT; 1028 AA.  
AC Q9UQ52;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Neural adhesion molecule NB-3.  
GN HNB-3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=98146168; PubMed=9486763;  
RX Kamei Y., Tsutsumi O., Taketani Y., Watanabe K.;  
RT "cDNA cloning and chromosomal localization of neural adhesion  
molecule, NB-3 in human."  
RL J. Neurosci. Res. 51:275-283 (1998).  
DR ENBL; AB003592; BAA82612.1; -  
DR HSSP; P20241; 1CFB.  
DR Genew; HGNC:2176; CNTN6.  
DR GO; GO:0007155; P:cell adhesion; TAS.

```

DR GO; GO:0007417; P:central nervous system development; TAS.
DR InterPro; IPR003439; ABC_transporter.
DR InterPro; IPR003961; FN_III-like.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00041; fn3; 4.
DR Pfam; PF00047; Ig; 6.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00408; IGC2; 5.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00835; IG_LIKE; 6.
DR Immunoglobulin domain.
SQ SEQUENCE 1028 AA; 113956 MW; 8B5A2ED229936A6 CRC64;

Query Match 44.4%; Score 52; DB 4; Length 1028;
Best Local Similarity 71.4%; Pred. No. 9.9;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 EGRTECVLSNLRGR 20
DB 292 EGFYECVAGNLRGR 305

RESULT 9
Q9AKX8 PRELIMINARY; PRT; 826 AA.
AC Q9AKX8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Legionella pneumophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=446;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=serogroup 1;
RX MEDLINE=21150471; PubMed=11251842;
RA Lueneberg B., Mayer B., Daryab N., Kooistra O., Zaehring U.,
RA Rohde M., Swanson J., Prosch M.;
RT "Chromosomal insertion and excision of a 30 kb instable genetic
RT element is responsible for phase variation of lipopolysaccharide and
RT other virulence determinants in Legionella pneumophila.";
RL Mol. Microbiol. 39:1259-1271 (2001).
DR EMBL; AJ277755; CAC33467.1; -.
KW Hypothetical protein.
SQ SEQUENCE 826 AA; 91581 MW; 4BD5404C2665CFEF CRC64;

Query Match 41.9%; Score 49; DB 2; Length 826;
Best Local Similarity 42.9%; Pred. No. 25;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 QRVEILGRTECVLSNLRGR 21
DB 782 RRAESNEGRLETTIESLKGRS 802

RESULT 10
P97528 PRELIMINARY; PRT; 1028 AA.
AC P97528;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NB-3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.

GO; GO:0007417; P:central nervous system development; TAS.
DR InterPro; IPR003439; ABC_transporter.
DR InterPro; IPR003961; FN_III-like.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00041; fn3; 4.
DR Pfam; PF00047; Ig; 6.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00408; IGC2; 5.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00835; IG_LIKE; 6.
DR Immunoglobulin domain.
SQ SEQUENCE 1028 AA; 113956 MW; 8B5A2ED229936A6 CRC64;

Query Match 44.4%; Score 52; DB 4; Length 1028;
Best Local Similarity 71.4%; Pred. No. 9.9;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 EGRTECVLSNLRGR 20
DB 292 EGFYECVAGNLRGR 305

RESULT 9
Q9AKX8 PRELIMINARY; PRT; 826 AA.
AC Q9AKX8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Legionella pneumophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=446;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=serogroup 1;
RX MEDLINE=21150471; PubMed=11251842;
RA Lueneberg B., Mayer B., Daryab N., Kooistra O., Zaehring U.,
RA Rohde M., Swanson J., Prosch M.;
RT "Chromosomal insertion and excision of a 30 kb instable genetic
RT element is responsible for phase variation of lipopolysaccharide and
RT other virulence determinants in Legionella pneumophila.";
RL Mol. Microbiol. 39:1259-1271 (2001).
DR EMBL; AJ277755; CAC33467.1; -.
KW Hypothetical protein.
SQ SEQUENCE 826 AA; 91581 MW; 4BD5404C2665CFEF CRC64;

Query Match 41.9%; Score 49; DB 2; Length 826;
Best Local Similarity 42.9%; Pred. No. 25;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 QRVEILGRTECVLSNLRGR 21
DB 782 RRAESNEGRLETTIESLKGRS 802

RESULT 10
P97528 PRELIMINARY; PRT; 1028 AA.
AC P97528;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NB-3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.

STRAIN=Wistar; TISSUE=Brain;
MEDLINE=97101230; PubMed=8945756;
Ogawa J., Kaneko H., Masuda T., Nagata S., Hosoya H., Watanabe K.;
RT "Novel neural adhesion molecules in the Contactin/F3 subgroup of the
RT immunoglobulin superfamily: Isolation and characterization of cDNAs
RT from rat brain.";
RL Neurosci. Lett. 218:173-176 (1996).
DR EMBL; D87248; BAA13320.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003439; ABC_transporter.
DR InterPro; IPR003961; FN_III-like.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00041; fn3; 4.
DR Pfam; PF00047; Ig; 6.
DR SMART; SM00060; FN3; 4.
DR SMART; SM00408; IGC2; 5.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00835; IG_LIKE; 6.
DR Immunoglobulin domain.
SQ SEQUENCE 1028 AA; 114065 MW; 47EFD8A370CF4923 CRC64;

Query Match 41.9%; Score 49; DB 11; Length 1028;
Best Local Similarity 71.4%; Pred. No. 32;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 EGRTECVLSNLRGR 20
DB 292 EGFYECVAGNLRGR 305

RESULT 11
Q9LPV7 PRELIMINARY; PRT; 428 AA.
AC Q9LPV7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE T23J18.14.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
RA Kim C., Altafi H., Bel O., Chin C., Chlou J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC T23J18 from chromosome
RT 1.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC011661; AAF16632.1; -.
SQ SEQUENCE 428 AA; 48982 MW; 603F3FF2725622F9 CRC64;

Query Match 41.0%; Score 48; DB 10; Length 428;
Best Local Similarity 45.5%; Pred. No. 18;
Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QRVEILGRTECVLSNLRGR 22
DB 132 KRQLENTTCLISITRGR 153

RESULT 12

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Q9JMB8 Q9JMB8 PRELIMINARY; PRT; 1028 AA.  
AC Q9JMB8;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Neural recognition molecule NB-3.  
GN CNTN6 OR MNB-3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129SVJ; TISSUE=Brain;  
RX MEDLINE=20183687; PubMed=10717476;  
RA Lee S., Takeda Y., Kawano H., Hosoya H., Nomoto M., Fujimoto D.,  
RA Takahashi N., Watanabe K.;  
RT "Expression and regulation of a gene encoding neural recognition  
RT molecule NB-3 of the contactin/f3 subgroup in mouse brain.";  
RL Gene 245:253-266 (2000).  
CC -1- SIMILARITY: CONTAINS 6 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
DR EMBL; AB032602; BA92367.1; -;  
DR HSSP; P20241; ICFB.  
DR MGD; MGI:1858223; Cntn6.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti...; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR003439; ABC\_TRANSPORTER\_1;  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR008957; FN\_III-like.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003598; Ig\_c2.  
DR Pfam; PF00041; fn3; 4.  
DR Pfam; PF00047; Ig; 6.  
DR SMART; SM00060; FN3; 4.  
DR SMART; SM00408; IGC2; 5.  
DR PROSITE; PS00211; ABC\_TRANSPORTER\_1; 1.  
DR PROSITE; PS00835; IG\_LIKE; 6.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW immunoglobulin domain.  
SQ SEQUENCE 1028 AA; 113759 MW; ABEC59F86CA3978F CRC64;  
  
Query Match 41.0%; Score 48; DB 11; Length 1028;  
Best Local Similarity 64.3%; Pred.No. 47;  
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
  
QY 7 EGRTECVLSNLRG 20  
Db 292 EGFYECIAGNLRG 305  
  
RESULT 13  
Q8C6X1 PRELIMINARY; PRT; 1028 AA.  
AC Q8C6X1;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Contactin 6.  
GN CNTN6.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Head;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573 (2002).  
DR EMBL; AK052972; BAC35227.1; -;  
DR MGD; MGI:1858223; Cntn6.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti...; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR003439; ABC\_TRANSPORTER\_1;  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR008957; FN\_III-like.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003598; Ig\_c2.  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF00041; fn3; 4.  
DR Pfam; PF00047; Ig; 6.  
DR SMART; SM00060; FN3; 4.  
DR SMART; SM00408; IGC2; 6.  
DR PROSITE; PS00211; ABC\_TRANSPORTER\_1; 1.  
DR PROSITE; PS00835; IG\_LIKE; 6.  
DR PROSITE; PS00290; IG\_MHC; 1.  
SQ SEQUENCE 1028 AA; 113761 MW; B233BD300881B101 CRC64;  
  
Query Match 41.0%; Score 48; DB 11; Length 1028;  
Best Local Similarity 64.3%; Pred.No. 47;  
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
  
QY 7 EGRTECVLSNLRG 20  
Db 292 EGFYECIAGNLRG 305  
  
RESULT 14  
Q94LS6 PRELIMINARY; PRT; 539 AA.  
AC Q94LS6;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=4530;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Nipponbare;  
RA Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,  
RA Brenner M., Burgess S., Hance M., Shvartsbeyn M., Teifrin T.,  
RA Riggs F., Hsiao J., Zismann V., Blunt S., Pai G., VanAken S.S.,  
RA Utterback T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L.,  
RA White O., Fraser C.M.;  
RT "Oryza sativa chromosome 10 BAC OSJNB0011A08 genomic sequence.";  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AC034258; AAKS4287.1; -;  
DR Gramene; Q94LS6; -;  
KW Hypothetical protein.  
SQ SEQUENCE 539 AA; 60201 MW; 8EBED40239310BC2 CRC64;  
  
Query Match 40.2%; Score 47; DB 10; Length 539;  
Best Local Similarity 56.2%; Pred.No. 34;  
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
  
QY 4 EILEGRTECVLSNLRG 19  
Db 9 EVHGRTRSCVLLNVRG 24  
  
RESULT 15

**Fri May 7 10:54:05 2004**

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Q7XDN4
ID Q7XDN4 PRELIMINARY; PRT; 539 AA.
AC Q7XDN4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OSJNB0011A08.11.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OC NCBI_TaxID=39947;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=cv. Nipponbare;
RC The Rice Chromosome 10 Sequencing Consortium;
RA "In-depth view of structure, activity, and evolution of rice
RT chromosome 10."
RL Science 300:1566-1569(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE017102; AAP54107.1; -.
KW Hypothetical protein.
SQ SEQUENCE 539 AA; 60201 MW; 8EBED40239310BC2 CRC64;

Query Match 40.2%; Score 47; DB 10; Length 539;
Best Local Similarity 56.2%; Pred. No. 34;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 4 EILFGRTECVLSNRG 19
| | | | |
Db 9 EVHEGTRSCVLLNVRG 24

Search completed: May 6, 2004, 12:46:18
Job time : 40 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 6, 2004, 12:40:41 ; Search time 11 Seconds  
(without alignments)  
108.874 Million cell updates/sec

Title: US-10-612-885A-1

Perfect score: 117

Sequence: 1 QRVLEGRTECVLSNLRGTRY 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	117	100.0	508	1	EPOR HUMAN
2	109	93.2	507	1	EPOR MOUSE
3	109	93.2	507	1	EPOR RAT
4	49	41.9	221	1	GIDB BIFLO
5	49	41.9	473	1	KRM1 MOUSE
6	49	41.9	475	1	KRM1 HUMAN
7	48	41.0	312	1	PYRB COREP
8	48	41.0	312	1	PYRB CORGL
9	47	40.2	956	1	TSF3 HUMAN
10	46	39.3	58	1	YS59 ENTFA
11	46	39.3	67	1	RS28 KLULA
12	46	39.3	67	1	RS28 KLUMA
13	46	39.3	489	1	CI28 MYCTU
14	46	39.3	697	1	AMS2 SCHPO
15	46	39.3	1609	1	YL54 CABEL
16	45.5	38.9	607	1	DB10 NICSY
17	45	38.5	512	1	YR33 MYCTU
18	45	38.5	1036	1	AX01 CHICK
19	44	37.6	473	1	KRM1 RAT
20	43.5	37.2	269	1	FPG VIBPA
21	43	36.8	486	1	MURC CORGL
22	43	36.8	956	1	TSF3 MOUSE
23	42.5	36.3	228	1	YAZ9 TREPA
24	42.5	36.3	1912	1	PTFD HUMAN
25	42	35.9	67	1	RS28 YEAST
26	42	35.9	365	1	DHAS YEAST
27	42	35.9	482	1	THII SALT1
28	42	35.9	482	1	THII SALT2
29	42	35.9	661	1	HCYC PANIN
30	42	35.9	1020	1	CONT MOUSE
31	42	35.9	1021	1	CONT RAT
32	41.5	35.5	1897	1	PTPF HUMAN
33	41	35.0	94	1	VE7 HPV37

34	41	35.0	200	1	RS4 THEVO
35	41	35.0	292	1	GLAXE ECOLI
36	41	35.0	346	1	XYNB THENE
37	41	35.0	413	1	PROA CAUCR
38	41	35.0	416	1	Y997 ARCFU
39	41	35.0	452	1	YHXY YEAST
40	41	35.0	479	1	PAX3 HUMAN
41	41	35.0	479	1	PAX3 MOUSE
42	41	35.0	520	1	PAX7 HUMAN
43	41	35.0	657	1	HS7F CABEL
44	41	35.0	833	1	DPOI THEFI
45	41	35.0	833	1	PTIA ECOLI

O37b95	thermoplasm
P77161	escherichia
Q60041	thermotoga
Q9a2x6	caulobacter
O29265	archaeoglob
P38867	saccharomyc
P23760	homo sapien
P24610	mus musculu
P23759	homo sapien
P11141	caenorhabdi
O52225	thermus fil
P32670	escherichia

## ALIGNMENTS

RESULT 1					
EPOR_HUMAN					
ID	EPOR_HUMAN	STANDARD;	PRT;	508 AA.	
AC	P19235;				
DT	01-NOV-1990 (Rel. 16, Created)				
DT	01-NOV-1990 (Rel. 16, Last sequence update)				
DT	15-MAR-2004 (Rel. 43, Last annotation update)				
DE	Erythropoietin receptor precursor (EPO-R).				
GN	EPOR.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=91372359; PubMed=1654273;				
RA	Enrenman K., St John T.;				
RT	"The erythropoietin receptor gene: cloning and identification of				
RT	multiple transcripts in an erythroid cell line OCIM1.";				
RL	Exp. Hematol. 19:973-977(1991).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=90304340; PubMed=2163696;				
RA	Jones S.S., D'Andrea A.D., Haines L.L., Wong G.G.;				
RT	"Human erythropoietin receptor: cloning, expression, and biologic				
RT	characterization.";				
RL	Blood 76:31-35(1990).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Placenta;				
RX	MEDLINE=92399733; PubMed=1668606;				
RA	Noguchi C.T., Bae K.S., Chin K., Wada Y., Schechter A.N.,				
RA	Hankins W.D.;				
RT	"Cloning of the human erythropoietin receptor gene.";				
RL	Blood 78:2548-2556(1991).				
RN	[4]				
RP	SEQUENCE OF 1-96 FROM N.A.				
RC	TISSUE=Placenta;				
RX	MEDLINE=92399734; PubMed=1668607;				
RA	Maouche L., Tournamille C., Hattab C., Boffa G., Cartron J.-P.,				
RA	Chretien S.;				
RT	"Cloning of the gene encoding the human erythropoietin receptor.";				
RL	Blood 78:2557-2563(1991).				
RN	[5]				
RP	SEQUENCE OF 1-17 FROM N.A.				
RX	MEDLINE=92147143; PubMed=1664413;				
RA	Penny L.A., Forget B.G.;				
RT	"Genomic organization of the human erythropoietin receptor gene.";				
RL	Genomics 11:974-980(1991).				
RN	[6]				
RP	PHOSPHORYLATION, AND INTERACTION WITH APS.				
RX	MEDLINE=99301417; PubMed=10374881;				
RA	Wakioka T., Sasaki A., Mitsui K., Yokouchi M., Inoue A., Komiya S.,				
RA	Yoshimura A.;				
RT	"APS, an adaptor protein containing pleckstrin homology (PH) and Src				
RT	homology-2 (SH2) domains inhibits the JAK-STAT pathway in				

RT collaboration with c-Cbl.";

RT Leukemia 13:760-767(1999).

RN [7]

RX X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 34-244.

RA MEDLINE=96291992; PubMed=86252530;

RA Livnah O., Stura E.A., Johnson D.L., Middleton S.A., Mulcahy L.S.,

RA Wrighton N.C., Dower W.J., Jolliffe L.K., Wilson I.A.;

RT "Functional mimicry of a protein hormone by a peptide agonist: the

RT EPO receptor complex at 2.8 A.";

RL Science 273:464-471(1996).

RN [8]

RX X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 34-244.

RA MEDLINE=99023198; PubMed=9808045;

RA Livnah O., Johnson D.L., Stura E.A., Farrell F.X., Barbone F.P.,

RA You Y., Liu K.D., Goldsmith M.A., He W., Krause C.D., Pestka S.,

RA Jolliffe L.K., Wilson I.A.;

RT "An antagonist peptide-EPO receptor complex suggests that receptor

RT dimerization is not sufficient for activation.";

RL Nat. Struct. Biol. 5:993-1004(1998).

RN [9]

RX X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 32-244 IN COMPLEX WITH EPO.

RA MEDLINE=98445092; PubMed=9774108;

RA Syed R.S., Reid S.W., Li C., Cheatham J.C., Aoki K.H., Liu B.,

RA Zhan H., Osslund T.D., Chirino A.J., Zhang J., Finer-Moore J.,

RA Elliott S., Sitney K., Katz B.A., Matthews D.J., Wendoloski J.J.,

RA Elgie J., Stroud R.M.;

RT "Efficiency of signalling through cytokine receptors depends

RT critically on receptor orientation.";

RL Nature 395:511-516(1998).

RN [10]

RX X-RAY CRYSTALLOGRAPHY (2.40 ANGSTROMS) OF 34-246.

RA MEDLINE=99141272; PubMed=9974392;

RA Livnah O., Stura E.A., Middleton S.A., Johnson D.L., Jolliffe L.K.,

RA Wilson I.A.;

RT "Crystallographic evidence for preformed dimers of erythropoietin

RT receptor before ligand activation.";

RL Science 283:987-990(1999).

CC -1- FUNCTION: Receptor for erythropoietin. Mediates erythropoietin-

CC induced erythroblast proliferation and differentiation. Upon EPO

CC stimulation, EPOR dimerizes triggering the JAK2/STAT5 signalling

CC cascade. Isoform 2 acts as a dominant-negative receptor of EPOR-

CC mediated signals.

CC -1- SUBUNIT: Interacts with APS.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors.

CC Subfamily 1.

CC -1- SIMILARITY: Contains 1 fibronectin type III domain.

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CC EMBL; M34986; AAA52401.1; -

CC EMBL; M60459; AAA52403.1; -

CC EMBL; S45332; AAB23271.1; -

CC EMBL; M76595; AAA52393.1; -

CC EMBL; M77244; AAA52392.1; -

CC PIR; A43799; ZUHUR.

CC PDB; 1EBP; 29-JUL-97.

CC PDB; 1EBA; 18-NOV-98.

CC PDB; 1EER; 01-OCT-99.

CC PDB; 1CNA; 11-AUG-99.

CC PDB; 1ERN; 07-JAN-00.

CC Genew; HGNC:3416; EPOR.

CC MIM; 133171; -

CC GO; GO:0005887; C:integral to plasma membrane; TAS.

CC GO; GO:0004900; F:erythropoietin receptor activity; TAS.

CC InterPro; IPR002996; CR1A.

CC InterPro; IPR008957; FN\_III-like.

DR InterPro; IPR003961; FN\_III.

DR InterPro; IPR003528; Hemtopoptn\_L\_F1.

DR Pfam; PF00041; fn3; 1.

DR PIRSF; PIRSF01959; EPO\_receptor; 1.

DR SMART; SM00060; FN3; 1.

DR PROSITE; PS01352; HEMATOPO REC L F1; 1.

KW Receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation;

KW 3D-structure.

FT SIGNAL 1 24

FT CHAIN 25 508

FT DOMAIN 25 250

FT TRANSMEM 251 273

FT DOMAIN 274 508

FT DOMAIN 148 213

FT SITE 368 368

FT DISULFID 52 62

FT DISULFID 91 107

FT MOD RES 368 368

FT CARBOHYD 76 76

FT HELIX 33 45

FT STRAND 51 54

FT STRAND 61 66

FT TURN 73 73

FT HELIX 74 76

FT STRAND 77 83

FT TURN 84 85

FT STRAND 89 90

FT STRAND 94 97

FT TURN 99 100

FT STRAND 103 108

FT HELIX 111 113

FT TURN 116 117

FT STRAND 120 126

FT TURN 127 128

FT STRAND 131 137

FT HELIX 139 141

FT STRAND 143 143

FT STRAND 149 155

FT STRAND 162 167

FT TURN 170 171

FT HELIX 175 177

FT STRAND 178 186

FT TURN 195 198

FT STRAND 200 201

FT STRAND 204 207

FT STRAND 215 224

FT TURN 226 228

FT STRAND 231 231

FT STRAND 240 243

SQ SEQUENCE 508 AA; 55065 MW; P9F326E162B9512A CRC64;

Query Match 100.0%; Score 117; DB 1; Length 508;

Best Local Similarity 100.0%; Pred. No. 8.3e-11;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QRVLEIGRTECVLSNLRGRTRY 23

Db 194 QRVLEIGRTECVLSNLRGRTRY 216

RESULT 2

ID EPOR MOUSE STANDARD; PRT; 507 AA.

AC P14753; O63852;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Erythropoietin receptor precursor (EPO-R).

GN EPOR.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_taxid=10090;



[1] SEQUENCE FROM N.A.  
 RP MEDLINE=89195238; PubMed=2539263;  
 RA D'Andrea A.D., Lodish H.F., Wong G.G.;  
 RT "Expression cloning of the murine erythropoietin receptor.";  
 RL Cell 57:277-285(1989).  
 [2] SEQUENCE FROM N.A.  
 RP STRAIN=BALB/c; TISSUE=Liver;  
 RC MEDLINE=91080149; PubMed=2175360;  
 RA Kuramochi S., Ikawa Y., Todokoro K.;  
 RT "Characterization of murine erythropoietin receptor genes.";  
 RL J. Mol. Biol. 216:567-575(1990).  
 [3] SEQUENCE FROM N.A.  
 RP MEDLINE=92017832; PubMed=1656233;  
 RA Hino M., Tojo A., Misawa Y., Morii H., Takaku F., Shibuya M.;  
 RT "Unregulated expression of the erythropoietin receptor gene caused by insertion of spleen focus-forming virus long terminal repeat in a murine erythroleukemia cell line.";  
 RL Mol. Cell. Biol. 11:5527-5533(1991).  
 [4] SEQUENCE OF 1-27 FROM N.A.  
 RP MEDLINE=90287158; PubMed=2162479;  
 RA Youssoufian H., Zon L.I., Orkin S.H., D'Andrea A.D., Lodish H.F.;  
 RT "Structure and transcription of the mouse erythropoietin receptor gene.";  
 RL Mol. Cell. Biol. 10:3675-3682(1990).  
 [5] SEQUENCE OF 1-24 FROM N.A.  
 RP MEDLINE=91201346; PubMed=1849897;  
 RA Lacombe C., Chretien S., Lemarchandel V., Mayeux P., Romeo P.H., Gisselbrecht S., Cartron J.-P.;  
 RT "Spleen focus-forming virus long terminal repeat insertional activation of the murine erythropoietin receptor gene in the T3C1-2 friend leukemia cell line.";  
 RL J. Biol. Chem. 266:6952-6956(1991).  
 [6] INTERACTION WITH APS.  
 RP MEDLINE=92510236; PubMed=12444928;  
 RA Wollberg P., Lennartsson J., Gottfridsson E., Yoshimura A., Ronstrand L.;  
 RT "The adapter protein APS associates with the multifunctional docking sites Tyr-568 and Tyr-936 in c-kit.";  
 RL Biochem. J. 370:1033-1038(2003).  
 [7] MUTAGENESIS.  
 RP MEDLINE=93180826; PubMed=8382775;  
 RA Miura O., Cleveland J.L., Ihle J.N.;  
 RT "Inactivation of erythropoietin receptor function by point mutations in a region having homology with other cytokine receptors.";  
 RL Mol. Cell. Biol. 13:1788-1795(1993).  
 CC -1- FUNCTION: Receptor for erythropoietin. Mediates erythropoietin-induced erythroblast proliferation and differentiation. Upon EPO stimulation, EPOR dimerizes triggering the JAK2/STAT5 signaling cascade. Isoform 2 acts as a dominant-negative receptor of EPOR-mediated signals.  
 CC -1- SUBUNIT: Interacts with APS.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors. Subfamily 1.  
 CC -1- SIMILARITY: Contains 1 fibronectin type III domain.  
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 DR EMBL; J04843; AAA37571.1; -;  
 DR EMBL; X53081; CAA37248.1; -;

DR EMBL; M38133; AAA37572.1; -;  
 DR EMBL; M62360; AAA37582.1; -;  
 DR EMBL; S59388; AAB20029.2; -;  
 DR PIR; A41686; A32385.  
 DR PIR; S14081; S14081.  
 DR HSSP; P19235; IEBB.  
 DR MGD; MGI:95408; EPOR.  
 DR InterPro; IPR002996; CRIA.  
 DR InterPro; IPR008957; FN III-like.  
 DR InterPro; IPR003961; FN III.  
 DR InterPro; IPR003528; Hemopoetn\_L\_P1.  
 DR Pfam; PF00441; fn3; 1.  
 DR FIRSF; FIRSF001959; EPO\_receptor; 1.  
 DR SMART; SM00060; FN3; 1.  
 DR PROSITE; PS01352; HEMATOPO REC L FL; 1.  
 KW Receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation.  
 FT SIGNAL 1 24  
 FT CHAIN 25 507 ERYTHROPOIETIN RECEPTOR.  
 FT DOMAIN 25 249 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 250 272 POTENTIAL.  
 FT DOMAIN 273 507 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 147 212 FIBRONECTIN TYPE-III.  
 FT SITE 367 367 APS-BINDING (BY SIMILARITY).  
 FT DISULFID 52 82 BY SIMILARITY.  
 FT DISULFID 90 106 BY SIMILARITY.  
 FT MOD RES 367 367 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 75 75 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CONFLICT 291 291 E -> D (IN REF. 3; AAB20029).  
 SQ SEQUENCE 507 AA; 55194 MW; 067657A2E26451CA CRC64;  
 Query Match 93.2%; Score 109; DB 1; Length 507;  
 Best Local Similarity 91.3%; Pred. No. 1.5e-09;  
 Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 QRVLELGRTGTECVLSNLRGTRY 23  
 DB 193 QRVLELGRTGTECVLSNLRGTRY 215  
 RESULT 3  
 ID EPOR\_RAT STANDARD; PRT; 507 AA.  
 AC Q07303;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Erythropoietin receptor precursor (EPO-R).  
 GN EPOR.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]\_TaxID=10116;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93266574; PubMed=7684373;  
 RA Masuda S., Nagao M., Takahata K., Konishi Y., Gallyas F., Tabira T., Sasaki R.;  
 RT "Functional erythropoietin receptor of the cells with neural characteristics. Comparison with receptor properties of erythroid cells.";  
 RL J. Biol. Chem. 268:11208-11216(1993).  
 CC -1- FUNCTION: Receptor for erythropoietin. Mediates erythropoietin-induced erythroblast proliferation and differentiation. Upon EPO stimulation, EPOR dimerizes triggering the JAK2/STAT5 signaling cascade. Isoform 2 acts as a dominant-negative receptor of EPOR-mediated signals.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors. Subfamily 1.  
 CC -1- SIMILARITY: Contains 1 fibronectin type III domain.  
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CC -----  
DR EMBL; D13566; BAA02761.1; -.  
DR PIR; A46713; A46713.  
DR HSSP; P19235; 1EBA.  
DR InterPro; IPR002996; CR1A.  
DR InterPro; IPR008957; FN\_III-like.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR003528; Hemopoptn\_L\_Ft.  
DR Pfam; PF00041; fn3; 1.  
DR PIRSF; PIRSF001959; EPO\_receptor; 1.  
DR SMART; SM00060; FN3; 1.  
DR PROSITE; PS01352; HEMATOPO\_REC\_L\_F1; 1.  
KW Receptor; Transmembrane; Glycoprotein; Signal.  
FT SIGNAL 1 24 BY SIMILARITY.  
FT CHAIN 25 507 ERYTHROPOIETIN RECEPTOR.  
FT DOMAIN 25 249 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 250 272 POTENTIAL.  
FT DOMAIN 273 507 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 147 212 FIBRONECTIN TYPE-III.  
FT DISULFID 52 62 BY SIMILARITY.  
FT DISULFID 90 106 BY SIMILARITY.  
FT CARBOHYD 75 75 N-LINKED (GLCNAC... ) (POTENTIAL).  
SQ SEQUENCE 507 AA; 55499 MW; AC79AF22D06A7312 CRC64;

Query Match 93.28; Score 109; DB 1; Length 507;  
Best Local Similarity 91.3%; Pred. No. 1.5e-09;  
Matches 21; Conservative 1; Mismatches -1; Indels 0; Gaps 0;

QY 1 QRVLEIGRTECVLSNLRGTRY 23  
DB 193 QRVLEIGRTECVLSNLRGGTRY 215

RESULT 4  
GIDB\_BIFLO STANDARD; PRT; 221 AA.  
AC QG6J4; 2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Methyltransferase gldb (EC 2.1.1.-) (Glucose inhibited division  
DE protein B).  
GN GIDB OR BL0646.  
OS Bifidobacterium longum.  
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;  
OC Bifidobacteriaceae; Bifidobacterium.  
OX NCBI\_TaxID=216816;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NCC 2705;  
RA Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,  
RA Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,  
RA Bridmore R.D., Arigoni F.  
RA "The genome sequence of Bifidobacterium longum reflects its adaptation  
RT to the human gastrointestinal tract".  
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).  
CC -1- FUNCTION: Probable S-adenosyl-L-methionine dependent  
CC methyltransferase specific for a sterol and/or lipid substrate (By  
CC similarity).  
CC -1- SIMILARITY: Belongs to the gldb family.

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CC -----  
DR EMBL; AB014686; AAN24468.1; -.  
DR HAMAP; MF\_00074; -; 1.  
DR InterPro; IPR003682; GidB.  
DR Pfam; PF02527; GidB; 1.  
DR ProDom; PD004441; GidB; 1.  
DR TIGRFAMs; TIGR00138; GidB; 1.  
KW Transferase; Methyltransferase; Complete proteome.  
SQ SEQUENCE 221 AA; 24163 MW; FB131A5126368A05 CRC64;

Query Match 41.9%; Score 49; DB 1; Length 221;  
Best Local Similarity 45.0%; Pred. No. 1.8;  
Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 QRVLEIGRTECVLSNLRG 20  
DB 120 QNVLEIGRSDAVIQVRKR 139

RESULT 5  
ID KRM1\_MOUSE STANDARD; PRT; 473 AA.  
AC Q99N43;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Kremen protein 1 precursor (Kringling-containing protein marking the eye  
DE and the nose) (Dickkopf receptor).  
GN KREMN1 OR KREMEN.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.; DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY.  
RC TISSUE=Brain, and Kidney;  
RX MEDLINE=21167372; PubMed=11267660;  
RA Nakamura T., Aoki S., Kitajima K., Takahashi T., Matsumoto K.,  
RA Nakamura T.;  
RT "Molecular cloning and characterization of Kremen, a novel  
RT kringling-containing transmembrane protein.";  
RL Biochim. Biophys. Acta 1518:63-72(2001).  
CC -1- FUNCTION: Receptor for Dickkopf protein. Cooperates with Dickkopf  
CC to block Wnt/beta-catenin signaling (By similarity).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
CC -1- TISSUE SPECIFICITY: In the adult, widely expressed with high  
CC levels in heart, lung, kidney, skeletal muscle and testis.  
CC -1- DEVELOPMENTAL STAGE: In the embryo, expression is first detected  
CC on day 9 and increases up to day 18. Lower levels are found in  
CC the telencephalon and the first brachial arch. At 10.5 dpc,  
CC ectodermal ridge (AER) of the developing fore- and hindlimb buds,  
CC expression is also observed in the myotome and in sensory tissues  
CC such as the nasal pit and optic vesicle.  
CC -1- SIMILARITY: Contains 1 CUB domain.  
CC -1- SIMILARITY: Contains 1 kringling domain.  
CC -1- SIMILARITY: Contains 1 WSC domain.

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CC EMBL; AB059617; BAB40968.1; -.  
CC HSSP; P00747; 1CEA.  
DR MGD; MGI:1933988; Kremen.  
DR GO; GO:0016021; C:integral to membrane; NAS.  
DR InterPro; IPR000859; CUB.  
DR InterPro; IPR000001; Kringling.





DR	PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
KW	Pyrimidine biosynthesis; Transferase; Complete proteome.
QY	SEQUENCE 312 AA; 33894 MW; F33154F4D03CF22 CRC64;
	Query Match 41.0%; Score 48; DB 1; Length 312;
	Best Local Similarity 61.1%; Pred. No. 3.7; Indels 0; Gaps 0;
	Matches 11; Conservative 1; Mismatches 6;
QY	4 EILEGRTECVLSNLRGRT 21
	:
Db	27 EVLEGREVKCLPTLRGRT 44
RESULT 9	
TSP3_HUMAN	STANDARD; PRT; 956 AA.
AC	P49746; Q8WV34;
DT	01-OCT-1996 (Rel. 34, Created)
DT	01-OCT-1996 (Rel. 34, Last sequence update)
DT	10-OCT-2003 (Rel. 42, Last annotation update)
DE	Thrombospondin 3 precursor.
GN	THBS3 OR TSP3.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCB1_TaxID=9606;
RX	[1]
RC	SEQUENCE FROM N.A.
RP	TISSUE=Lung;
RX	MEDLINE=96044440; PubMed=7558000;
RT	Adolph K.W., Long G.L., Winfield S., Ginns E.I., Bornstein P.;
RT	"Structure and organization of the human thrombospondin 3 gene
RT	(THBS3).";
RL	Genomics 27:329-336(1995).
RN	[2]
RN	SEQUENCE OF 1-736 FROM N.A.
RX	MEDLINE=97474796; PubMed=9331372;
RT	Winfield S.L., Tayebi N., Martin B.M., Ginns E.I., Sidransky E.;
RT	"Identification of three additional genes contiguous to the
RT	glucocerebrosidase locus on chromosome 1q21: implications for Gaucher
RT	disease.";
RL	Genome Res. 7:1020-1026(1997).
RN	[3]
RN	SEQUENCE OF 365-956 FROM N.A.
RX	TISSUE=Retina;
RX	MEDLINE=22388257; PubMed=12477932;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.
RA	Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.P., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Diatchenko L., Marusina K., Farmer A.M., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Uesdin T.B., Toohiyuki S., Carninci P., Prange C.
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Vallalon D.K., Muzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA	Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length
RT	human and mouse cDNA sequences.";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC	-!- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and
CC	cell-to-matrix interactions. Can bind to fibrinogen, fibronectin,
CC	laminin and type V collagen.
CC	-!- SUBUNIT: Oligomer; disulfide-linked.
CC	-!- SIMILARITY: Belongs to the thrombospondin family.
CC	-!- SIMILARITY: Contains 4 EGF-like domains.
CC	-!- SIMILARITY: Contains 7 TSP type-3 domains.

DR	PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
KW	Pyrimidine biosynthesis; Transferase; Complete proteome.
QY	SEQUENCE 312 AA; 33894 MW; F33154F4D03CF22 CRC64;
	Query Match 41.0%; Score 48; DB 1; Length 312;
	Best Local Similarity 61.1%; Pred. No. 3.7;
	Matches 11; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY	4 EILEGRTECVLSNLRGRT 21
	:
Db	27 EVLEGREVKCLPTLRGRT 44
RESULT 9	
TSP3_HUMAN	STANDARD; PRT; 956 AA.
AC	P49746; Q8WV34;
DT	01-OCT-1996 (Rel. 34, Created)
DT	01-OCT-1996 (Rel. 34, Last sequence update)
DT	10-OCT-2003 (Rel. 42, Last annotation update)
DE	Thrombospondin 3 precursor.
GN	THBS3 OR TSP3.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCB1_TaxID=9606;
RX	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Lung;
RX	MEDLINE=96044440; PubMed=7558000;
RT	Adolph K.W., Long G.L., Winfield S., Ginns E.I., Bornstein P.;
RT	"Structure and organization of the human thrombospondin 3 gene
RL	(THBS3).";
RL	Genomics 27:329-336(1995).
RP	[2]
RP	SEQUENCE OF 1-736 FROM N.A.
RX	MEDLINE=97474796; PubMed=9331372;
RT	Winfield S.L., Tayebi N., Martin B.M., Ginns E.I., Sidransky E.;
RT	"Identification of three additional genes contiguous to the
RT	glucocerebrosidase locus on chromosome 1q21: implications for Gaucher
RL	disease.";
RL	Genome Res. 7:1020-1026(1997).
RP	[3]
RP	SEQUENCE OF 365-956 FROM N.A.
RX	TISSUE=Retina;
RX	MEDLINE=22388257; PubMed=12477932;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.
RA	Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.P., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Diatchenko L., Marusina K., Farmer A.M., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Uesdin T.B., Toohiyuki S., Carninci P., Prange C.
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Vallalon D.K., Muzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailis D.E.,
RA	Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length
RT	human and mouse cDNA sequences.";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC	-!- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and
CC	cell-to-matrix interactions. Can bind to fibrinogen, fibronectin,
CC	laminin and type V collagen.
CC	-!- SUBUNIT: Oligomer; disulfide-linked.
CC	-!- SIMILARITY: Belongs to the thrombospondin family.
CC	-!- SIMILARITY: Contains 4 EGF-like domains.
CC	-!- SIMILARITY: Contains 7 TSP type-3 domains.

```

FT DISULFID      715   936    BY SIMILARITY.
FT CARBOHYD     310   310    N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD     407   407    N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD     644   644    N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD     937   937    N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE     956 AA; 104201 MW; A59B136DF0FFES8 CRC64;

Query Match          40.2%; Score 47; DB 1; Length 956;
Best Local Similarity 45.5%; Pred. No. 18;
Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QRVLEIGRTECVLSNLRGTR 22
DB 113 QQAGLADGRTHTVLLRLGPSR 134
       |.:|::|||::|::|:|
RESULT 10
IID YS59 ENTPA STANDARD; PRT; 58 AA.
Q830C9;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DN Probable tautomerase EF2859 (EC 5.3.2.-).
GN EF2859.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxId=1351;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=V583 / ATCC 700802;
RC MEDLINE=22550857; PubMed=12663927;
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
RA Tetzelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,
RA Vamathevan J., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,
RA Vamatheswaran S., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
RA Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
RA "Role of mobile DNA in the evolution of vancomycin-resistant
RT Enterococcus faecalis";
RT Science 299:2071-2074(2003).
RL -1- SIMILARITY: Belongs to the tautomerase family.
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; AE016956; AAC82551.1; -.
DR TIGR; EF2859; -.
DR HAMAP; MF 00718; -.
DR InterPro; IPR004370; Taut.
DR Pfam; PF01361; Tautomerase; 1.
DR ProDom; PD404143; Taut; 1.
DR IsoMase; Complete proteome.
KW INIT MET 0 0
FT INIT SITE 1 1
SQ SEQUENCE 58 AA; 6589 MW;
BY SIMILARITY.
CATALYTIC BASE (BY SIMILARITY).
FAE19A0C5D93CE4E CRC64;

Query Match          39.3%; Score 46; DB 1; Length 58;
Best Local Similarity 60.0%; Pred. No. 1.2;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 VEILEGRTECVLSNL 17
DB 5 VELIEGRTEQLTNW 19
       ||::|||::|::|:|
RESULT 11
RS28 KLULA
```

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch))

DR EMBL; X69583; CAA49297.1; --  
 DR PIR; S30006; S30006.  
 DR InterPro; IPR000289; Ribosomal\_S28e.  
 DR Pfam; PF01200; Ribosomal\_S28e; 1.  
 DR ProDom; PD005541; Ribosomal\_S28e; 1.  
 DR PROSITE; PS00961; RIBOSOMAL\_S28E; 1.  
 KW Ribosomal protein.  
 SQ SEQUENCE 67 AA; 7522 MW; 51E58353F18A131 CRC64;

Query Match 39.3%; Score 46; DB 1; Length 67;  
 Best Local Similarity 42.9%; Pred. No. 1.4;  
 Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 RVEILGRTECVLSNLGRTR 22  
 ||| ||| : : : |||  
 Db 29 RVEPLEDTRTRVNRKGPVR 49

## RESULT 13

C128 MYCTU STANDARD; PRT; 489 AA.  
 AC Q59572;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Putative cytochrome P450 128 (EC 1.14.-.-).  
 GN CYP128 OR RV2268C OR WT2330 OR MTCY339.42 OR MB2291C.  
 OS Mycobacterium tuberculosis, and  
 OS Mycobacterium bovis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1773, 1765;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=M.tuberculosis; STRAIN=H37Rv;  
 RX MEDLINE=98295987; PubMed=9634230;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,  
 Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holtroyd S.,  
 Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
 Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
 Sulston J.E., Taylor K., Whitehead S., Barrall B.G.;  
 RA "Deciphering the biology of Mycobacterium tuberculosis from the  
 RT complete genome sequence."  
 RL Nature 393:537-544 (1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;  
 RX MEDLINE=22206494; PubMed=12218036;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,  
 Kolonay J.F., Nelson W.C., Umayam L.A., Ernolova M., Salzberg S.L.,  
 Delcher A.L., Uitterlbeck T., Weidman J., Khouri H., Gill J., Mikula A.,  
 Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;  
 RA "Whole-genome comparison of Mycobacterium tuberculosis clinical and  
 RT laboratory strains."  
 RL J. Bacteriol. 184:5479-5490 (2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=M.bovis; STRAIN=AF2122/97;  
 RX MEDLINE=22709107; PubMed=12788972;  
 RA Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,  
 Pryor M., Duthoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,  
 Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,  
 Parkhill J., Barrall B.G., Cole S.T., Gordon S.V., Hewinson R.G.;  
 RA "The complete genome sequence of Mycobacterium bovis."  
 RT Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: Belongs to the cytochrome P450 family.  
 CC -----  
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DR EMBL; Z77163; CAB00967.1; --  
 DR EMBL; AE007076; AAK46612.1; --  
 DR EMBL; BX248342; CAD97152.1; --  
 DR PIR; H70729; H70729.  
 DR HSP; Q00441; 10XA.  
 DR TIGR; MT2330; --  
 DR Tuberculin; RV2268c; --  
 DR InterPro; IPR001128; Cytochrome\_P450.  
 DR Pfam; PF00067; P450; 1.  
 DR PRINTS; PR00385; P450.  
 DR PROSITE; PS00086; CYTOCHROME\_P450; 1.  
 KW Hypothetical protein; Oxidoreductase; Monooxygenase; Heme;  
 KW Transmembrane; Complete proteome.  
 FT TRANSMEM 207 227 POTENTIAL.  
 FT TRANSMEM 256 276 POTENTIAL.  
 FT TRANSMEM 315 335 POTENTIAL.  
 FT TRANSMEM 383 403 POTENTIAL.  
 FT METAL 435 435 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).  
 SQ SEQUENCE 489 AA; 53313 MW; 633F233CEP03AD7A CRC64;

Query Match 39.3%; Score 46; DB 1; Length 489;  
 Best Local Similarity 47.6%; Pred. No. 13;  
 Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 RVEILGRTECVLSNLGRTR 22  
 ||| ||| : : : |||  
 Db 458 RIEVBPPTWTNANLRLTR 478

## RESULT 14

AMS2 SCHPO STANDARD; PRT; 697 AA.  
 ID AMS2 SCHPO  
 AC Q9UR74; Q9P721;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE CENP-A multicopy suppressor protein 2.  
 GN AMS2 OR SPCC290.04 OR SPCC4F11.01.  
 OS Schizosaccharomyces pombe (Pission Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RX MEDLINE=21848401; PubMed=11859360;  
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
 RA Spouris J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,  
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,  
 RA Gentles S., Geble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,  
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,  
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
 RA Gabel C., Fuchs M., Pritsch C., Holzer E., Moestl D., Hilbert H.,

```

RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Pavello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins I., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Lathrelle P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
RA Sims M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RT RT
RL Nature 368:32-38(1994).
CC CC
CC -1- SIMILARITY: TO HUMAN KIAA0152.
CC CC
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CC CC
CC EMBL; L23646; AAA28040.1; -.
CC PIR; S4821; S4821.
CC HSPSP; P01130; 1AJJ.
CC Wormpmp; F44E2.4; CE00182.
CC Pfam; PF00057; 1dl_recept_a; 1.
CC SMART; SM00192; LDLa; 1.
CC DR
CC Hypothetical protein.
CC KW
CC SSSEQUENCE 1609 AA; 175966 MW; 4AE845E2AD2207CB CRC64;
CC
CC Query Match 39.3%; Score 46; DB 1; Length 1609;
CC Best Local Similarity 56.7%; Pred.No. 47;
CC Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
CC
CC QY 5 ILGRTGTCVLN 16
CC DB 877 LLGRTSCVSS 888
CC
CC Search completed: May 6, 2004, 12:45:26
CC Job time : 12 secs

```



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 6, 2004, 12:44:02 ; Search time 21 Seconds  
(without alignments)  
105.353 Million cell updates/sec

Title: US-10-612-885A-1

Perfect score: 117

Sequence: 1 QRVLEGRTECVLSNLRGTRY 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_78.\*

1: PIR1.\*

2: PIR2.\*

3: PIR3.\*

4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	117	100.0	508	1 ZUHUR	erythropoietin rec
2	109	93.2	265	2 S14081	erythropoietin rec
3	109	93.2	507	1 A32385	erythropoietin rec
4	109	93.2	507	1 A46713	erythropoietin rec
5	47	40.2	956	2 A57121	thrombospondin 3 p
6	46	39.3	67	2 S30006	ribosomal protein
7	46	39.3	67	2 S30005	probable DNA-bind
8	46	39.3	288	2 T30648	cytochrome P450 Rv
9	46	39.3	489	1 H70729	probable transcript
10	46	39.3	710	2 T41352	F4E2.4 protein -
11	46	39.3	1609	2 S44821	ATP-dependent RNA
12	45.5	38.9	607	1 S42639	probable transmem
13	45	38.5	316	2 D83406	hypothetical prote
14	45	38.5	512	1 D70506	axinin 1 precursor
15	45	38.5	1036	2 S22383	protein PV100 [imp
16	44.5	38.0	810	2 T44430	30S ribosomal prot
17	44	37.6	47	2 AB0673	hypothetical prote
18	44	37.6	195	2 AE1823	degenerate transpo
19	43	36.8	84	2 C97955	hypothetical prote
20	43	36.8	408	2 A87649	IS1167, transposas
21	43	36.8	418	2 C95184	IS1167, transposas
22	43	36.8	418	2 F95096	hypothetical prote
23	43	36.8	654	2 S76870	transferrin-bindin
24	43	36.8	931	2 S66574	thrombospondin 3 -
25	43	36.8	956	1 A46016	probable protein-t
26	43	36.8	1437	2 T31093	hypothetical prote
27	42.5	36.3	1232	2 H71251	protein-tyrosine-p
28	42.5	36.3	1894	2 C54689	protein-tyrosine-p
29	42.5	36.3	1912	2 A56178	

30 42 35.9 67 1 R3BY33 ribosomal protein  
31 42 35.9 67 2 S51401 ribosomal protein  
32 42 35.9 231 2 T49830 hypothetical prote  
33 42 35.9 255 2 A37877 transposase (orf2)  
34 42 35.9 260 2 C98084 degenerate transpo  
35 42 35.9 283 2 S75226 esterase elr1916 -  
36 42 35.9 322 2 D89785 hypothetical prote  
37 42 35.9 365 2 J00198 aspartate-semialde  
38 42 35.9 418 2 A95168 IS1167, transposas  
39 42 35.9 418 2 B95197 IS1167, transposas  
40 42 35.9 418 2 B95146 IS1167, transposas  
41 42 35.9 418 2 H95208 IS1167, transposas  
42 42 35.9 482 2 T46944 thiamin biosynthes  
43 42 35.9 482 2 A10554 thiamin biosynthes  
44 42 35.9 514 2 T29652 inward rectifier p  
45 42 35.9 562 2 E70399 hydrogenase regula

#### ALIGNMENTS

##### RESULT 1

ZUHUR

erythropoietin receptor precursor - human

C:Species: Homo sapiens (man)

C:Date: 12-Feb-1993 #sequence revision 05-Apr-1995 #text change 22-Jun-1999

C:Accession: A43799; A60160; A49824; A53958; A53280; I52563

R:Jones, S.S.; D'Andrea, A.D.; Haines, L.L.; Wong, G.G.

Blood 76, 31-35, 1990

A:Title: Human erythropoietin receptor: cloning, expression, and biologic characterizat

A:Reference number: A43799; MUID:90304340; PMID:2163696

A:Accession: A43799

A:Molecule type: mRNA

A:Residues: 1-508 <JON>

A:Cross-references: GB:M60459; NID:g182244; PIDN:AAA52403.1; PID:g182245

R:Winkelmann, J.C.; Penny, L.A.; Deaven, L.L.; Forget, B.G.; Jenkins, R.B.

Blood 76, 24-30, 1990

A:Title: The gene for the human erythropoietin receptor: analysis of the coding sequenc

A:Reference number: A60160; MUID:90304334; PMID:2163695

A:Accession: A60160

A>Status: not compared with conceptual translation

A:Molecule type: mRNA; DNA

A:Residues: 1-101, 'R', 103-188, 'RP', 191-243, 'E', 245-508 <WIN>

R:Nozuchi, C.T.; Bae, K.S.; Chin, K.; Wada, Y.; Schechter, A.N.; Hankins, W.D.

Blood 78, 2548-2556, 1991

A:Title: Cloning of the human erythropoietin receptor gene.

A:Reference number: A49824; MUID:92399733; PMID:1668606

A:Accession: A49824

A:Molecule type: DNA

A:Residues: 1-508 <NOG>

A:Cross-references: GB:S45332; NID:G255496; PIDN:AAB23271.1; PID:G255497

A:Experimental source: Placenta

A:Note: sequence extracted from NCBI backbone (NCBIN:113293, NCBIP:113294)

R:Erhman, K.; St. John, T.

Exp. Hematol. 19, 973-977, 1991

A:Title: The erythropoietin receptor gene: cloning and identification of multiple trans

A:Reference number: A53958; MUID:91372359; PMID:1654273

A:Accession: A53958

A:Molecule type: mRNA

A:Residues: 1-508 <EHR>

R:Penny, L.A.; Forget, B.G.

Genomics 11, 974-980, 1991

A:Title: Genomic organization of the human erythropoietin receptor gene.

A:Reference number: A55280; MUID:92147143; PMID:1664413

A:Accession: A55280

A:Molecule type: DNA

A:Residues: 1-17, 381-387, 'LLEQQQDA', 391-395; 504-508 <PEN>

A:Note: sequence modified after extraction from NCBI backbone

A:Note: the authors translated the codon GAT for residue 31 as B

R:Maouche, L.; Tournamille, C.; Hattab, C.; Boffa, G.; Carttron, J.P.; Chretien, S.

Blood 78, 2557-2563, 1991

A:Title: Cloning of the gene encoding the human erythropoietin receptor.

A;Reference number: I52563; MUID:92399734; PMID:1668607  
A;Accession: I52563  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-96 <RES>  
A;Cross-references: GB:M76595; NID:g182147; PIDN:AAA52393.1; PID:g553281  
C;Genetics:  
A;Gene: GDB:EPOR  
A;Cross-references: GDB:I25242; OMIM:133171  
A;Map position: 19p13.3-19p13.2  
A;Introns: 39/1; 84/2; 143/1; 195/3; 247/1; 276/2; 305/3  
A;Superfamily: erythropoietin receptor; cytokine receptor; glycoprotein; transmembrane protein  
C;Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein  
F;1-24/Domain: signal sequence #status predicted <SIG>  
F;25-508/Product: erythropoietin receptor #status predicted <MAT>  
F;52-250/Domain: extracellular #status predicted <EXT>  
F;53-239/Domain: cytochrome motif  
F;233-237/Region: WSXWS motif  
F;231-272/Domain: transmembrane #status predicted <TM>  
F;273-508/Domain: intracellular #status predicted <INT>  
F;52-62.91-107/Disulfide bonds: #status predicted  
F;76/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 117; DB 1; Length 508;  
Best Local Similarity 100.0%; Pred. No. 2.6e-10;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRVLEGRTECVLSNLRGTRY 23  
|||||  
Db 194 QRVLEGRTECVLSNLRGTRY 216  
|||||

RESULT 2  
S14081  
erythropoietin receptor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
A;Accession: S14081; I49653  
R;Kuramochi, S.; Ikawa, Y.; Todokoro, K.  
J. Mol. Biol. 216, 567-575, 1990  
A;Title: Characterization of murine erythropoietin receptor genes.  
A;Reference number: S13249; MUID:91080149; PMID:2175360  
A;Accession: S14081  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-265 <RES>  
R;Lacombe, C.; Chretien, S.; Lemarchandel, V.; Mayeux, P.; Romeo, P.  
J. Biol. Chem. 266, 6952-6956, 1991  
A;Title: Spleen focus-forming virus long terminal repeat insertional activation of the m  
A;Reference number: I49653; MUID:91201346; PMID:1849897  
A;Accession: I49653  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-24 <RES>  
A;Cross-references: GB:M62360; NID:g193199; PIDN:AAA37582.1; PID:g193200  
C;Superfamily: erythropoietin receptor; cytokine receptor; glycoprotein; transmembrane protein  
C;Keywords: cytokine receptor; transmembrane protein  
F;52-238/Domain: cytokine receptor homology <CRS>

Query Match 93.2%; Score 109; DB 2; Length 265;  
Best Local Similarity 91.3%; Pred. No. 2.3e-09;  
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QRVLEGRTECVLSNLRGTRY 23  
|||||  
Db 193 QRVLEGRTECVLSNLRGTRY 215  
|||||

RESULT 3  
A32385  
erythropoietin receptor precursor, membrane-bound form - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 28-Sep-1990 #sequence\_revision 05-Apr-1995 #text\_change 22-Jun-1999

C;Accession: A41686; A32385; S13249  
R;Hino, M.; Tojo, A.; Misawa, Y.; Morii, H.; Takaku, F.; Shibuya, M.  
Mol. Cell. Biol. 11, 5527-5533, 1991  
A;Title: Unregulated expression of the erythropoietin receptor gene caused by insertion  
A;Reference number: A41686; MUID:92017832; PMID:1656233  
A;Accession: A41686  
A;Molecule type: mRNA  
A;Residues: 1-507 <HIN>  
A;Cross-references: GB:S59388; NID:g237036; PIDN:AA20029.1; PID:g237037  
A;Experimental source: murine erythrocytopenia (MEL) cell line F5-5  
R;D'Andrea, A.D.; Lodish, H.F.; Wong, G.G.  
Cell 57, 277-285, 1989  
A;Title: Expression cloning of the murine erythropoietin receptor.  
A;Reference number: A32385; MUID:89195238; PMID:2539263  
A;Accession: A32385  
A;Molecule type: mRNA  
A;Residues: 1-507 <DB>  
A;Cross-references: GB:J04843; NID:g193090; PIDN:AAA37571.1; PID:g309219  
A;Experimental source: murine erythrocytopenia (MEL) cells, subclone 745  
R;Kuramochi, S.; Ikawa, Y.; Todokoro, K.  
J. Mol. Biol. 216, 567-575, 1990  
A;Title: Characterization of murine erythropoietin receptor genes.  
A;Reference number: S13249; MUID:91080149; PMID:2175360  
A;Accession: S13249  
A;Molecule type: DNA; mRNA  
A;Residues: 1-507 <KUR>  
A;Cross-references: EMBL:X53081; NID:g50861; PIDN:CAA37248.1; PID:g50862  
A;Experimental source: murine erythrocytopenia K-1 cells  
C;Genetics:  
A;Introns: 39/1; 83/2; 142/1; 194/3; 246/1; 275/2; 304/3  
C;Superfamily: erythropoietin receptor; cytokine receptor; glycoprotein; transmembrane protein  
C;Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein  
F;1-24/Domain: signal sequence #status predicted <SIG>  
F;25-507/Product: erythropoietin receptor #status predicted <MAT>  
F;25-249/Domain: extracellular #status predicted <EXT>  
F;252-238/Domain: cytokine receptor homology <CRS>  
F;250-271/Domain: transmembrane #status predicted <TM>  
F;272-507/Domain: intracellular #status predicted <INT>  
F;52-62.90-106/Disulfide bonds: #status predicted  
F;75/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 93.2%; Score 109; DB 1; Length 507;  
Best Local Similarity 91.3%; Pred. No. 4.6e-09;  
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QRVLEGRTECVLSNLRGTRY 23  
|||||  
Db 193 QRVLEGRTECVLSNLRGTRY 215  
|||||

RESULT 4  
A46713  
erythropoietin receptor precursor - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Jun-2000  
C;Accession: A46713  
R;Masuda, S.; Nagao, M.; Takahata, K.; Konishi, Y.; Gallyas Jr., F.; Tabira, T.; Sasaki  
J. Biol. Chem. 268, 11208-11216, 1993  
A;Title: Functional erythropoietin receptor of the cells with neural characteristics. C  
A;Reference number: A46713; MUID:93266574; PMID:7684373  
A;Accession: A46713  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-507 <MAS>  
A;Cross-references: GB:D13566; NID:g286209; PIDN:BAA02761.1; PID:g286210  
A;Experimental source: PC12 and erythroid cells  
A;Note: sequence extracted from NCBI backbone (NCBI:132811, NCBIP:132813)  
C;Superfamily: erythropoietin receptor; cytokine receptor; glycoprotein; transmembrane protein  
C;Keywords: cytokine receptor; glycoprotein; transmembrane protein  
F;1-24/Domain: signal sequence #status predicted <SIG>  
F;25-507/Product: erythropoietin receptor #status predicted <MAT>  
F;25-249/Domain: extracellular #status predicted <EXT>  
F;52-238/Domain: cytokine receptor homology <CRS>

F;250-271/Domain: transmembrane #status predicted <TM>  
 F;272-507/Domain: intracellular #status predicted <INT>  
 F;75/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 93.2%; Score 109; DB 1; Length 507;  
 Best Local Similarity 91.3%; Pred. No. 4.6e-09;  
 Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QRVLEIGRTCEVLSNLRGRTY 23  
 |||||  
 DB 193 QRVLEIGRTCEVLSNLRGGTRY 215

## RESULT 5

A57121  
 ribosomopondin 3 precursor - human  
 C:Species: Homo sapiens (man)  
 C>Date: 03-Nov-1995 #sequence\_revision 03-Nov-1995 #text\_change 21-Jan-2000  
 C:Accession: A57121; T08830  
 R:Adolph, K.W.; Long, G.L.; Winfield, S.; Ginns, E.I.; Bornstein, P.  
 Genomics 27, 329-336, 1995  
 A>Title: Structure and organization of the human thrombospondin 3 gene (THBS3).  
 A:Reference number: A57121; MUID:96044440; PMID:7558000  
 A:Accession: A57121  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-956 <ADO>  
 A:Cross-references: GB:138969; NID:g886298; PIDN:AAC41762.1; PID:g886299; GB:L38970  
 R:Winfield, S.L.; Tayebi, N.; Martin, B.M.; Ginns, E.I.; Sidransky, E.  
 Genome Res. 7, 1020-1026, 1997  
 A>Title: Identification of three additional genes contiguous to the glucocerebrosidase 1  
 A:Reference number: Z16482; MUID:97474796; PMID:9331372  
 A:Accession: T08830  
 A>Status: translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-736 <MIN>  
 A:Cross-references: EMBL:AF023268; NID:g2564910; PIDN:AAC51818.1; PID:g2564912  
 C:Genetics:  
 A:Gene: GDB:THBS3  
 A:Cross-references: GDB:409953; OMIM:188062  
 A:Map position: 1q21-q23  
 A:Introns: 27/1; 96/1; 181/3; 216/1; 225/1; 256/1; 270/1; 319/3; 366/3; 392/3; 443/3; 48  
 C:Function:  
 A:Description: mediates cell-to-matrix and cell-to-cell interactions  
 C:Superfamily: thrombospondin 3; EGF homology  
 P:374-412/Domain: EGF homology <EGF>

Query Match 40.2%; Score 47; DB 2; Length 956;  
 Best Local Similarity 45.5%; Pred. No. 41;  
 Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QRVLEIGRTCEVLSNLRGRTY 22  
 |||||  
 DB 113 QOAGLADGKTHVLLRLGSPR 134

## RESULT 6

S30006  
 ribosomal protein S28.e - yeast (Kluyveromyces marxianus)  
 N:Alternate names: ribosomal protein YS33  
 C:Species: Kluyveromyces marxianus  
 C>Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 07-May-1999  
 C:Accession: S30006  
 R:Hoekstra, R.; Ferreira, P.M.; Bootsman, T.C.; Mager, W.H.; Planta, R.J.  
 Yeast 8, 949-959, 1992  
 A>Title: Structure and expression of the ABF1-regulated ribosomal protein S33 gene in Kl  
 A:Reference number: S30005; MUID:93127729; PMID:1481571  
 A:Accession: S30006  
 A:Molecule type: DNA  
 A:Residues: 1-67 <HOE>  
 A:Cross-references: GB:S52656  
 C:Genetics:  
 A:Gene: S33

C:Superfamily: rat ribosomal protein S28  
 C:Keywords: protein biosynthesis; ribosome

Query Match 39.3%; Score 46; DB 2; Length 67;  
 Best Local Similarity 42.9%; Pred. No. 3.7;  
 Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 RVEILEGRTCEVLSNLRGRTY 22  
 |||||  
 DB 29 RVEFLEDTRTIVRNKGPVR 49

## RESULT 7

S30005  
 ribosomal protein S28.e - yeast (Kluyveromyces marxianus var. lactis)  
 N:Alternate names: ribosomal protein YS33  
 C:Species: Kluyveromyces marxianus var. lactis, Candida sphaerica  
 C>Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 07-May-1999  
 C:Accession: S30005  
 R:Hoekstra, R.; Ferreira, P.M.; Bootsman, T.C.; Mager, W.H.; Planta, R.J.  
 Yeast 8, 949-959, 1992  
 A>Title: Structure and expression of the ABF1-regulated ribosomal protein S33 gene in K  
 A:Reference number: S30005; MUID:93127729; PMID:1481571  
 A:Accession: S30005  
 A:Molecule type: DNA  
 A:Residues: 1-67 <HOE>  
 A:Cross-references: GB:S53420  
 C:Genetics:  
 A:Gene: S33  
 C:Superfamily: rat ribosomal protein S28  
 C:Keywords: protein biosynthesis; ribosome

Query Match 39.3%; Score 46; DB 2; Length 67;  
 Best Local Similarity 42.9%; Pred. No. 3.7;  
 Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 RVEILEGRTCEVLSNLRGRTY 22  
 |||||  
 DB 29 RVEFLEDTRTIVRNKGPVR 49

## RESULT 8

T30648  
 probable DNA-binding protein 46L - Molluscum contagiosum virus 1  
 N:Alternate names: MC046L  
 C:Species: Molluscum contagiosum virus 1  
 C>Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 27-Oct-2003  
 C:Accession: T30648  
 R:Senkevich, T.G.; Bugert, J.J.; Staler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.  
 Science 273, 813-816, 1996  
 A>Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host re  
 A:Reference number: Z20876; MUID:96325459; PMID:8670425  
 A:Accession: T30648  
 A>Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-288 <SEN>  
 A:Cross-references: EMBL:U60315; NID:gl491943; PIDN:AAC55174.1; PID:gl491989  
 C:Genetics:  
 A:Note: MC046L  
 C:Superfamily: DNA-binding phosphoprotein, vaccinia I3L type  
 C:Keywords: DNA binding

Query Match 39.3%; Score 46; DB 2; Length 288;  
 Best Local Similarity 66.7%; Pred. No. 17;  
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 11 ECVLNLRGRTY 22  
 |||||  
 DB 133 ECIVNLRGGTR 144

## RESULT 9

H70729

A:Molecule type: DNA  
A:Residues: 1-1609 <AND>  
A:Cross-references: EMBL:123646; NID:9388595; PID:9388601  
C:Genetics:  
C:Introns: 107/2; 173/2; 228/3; 594/3; 1165/2; 1216/3; 1231/3; 1258/2; 1300/2; 1321/3; 1  
C:Superfamily: LDL receptor ligand-binding repeat homology  
C:Full-45/Domain: LDL receptor ligand-binding repeat homology <LDL>  
  
Query Match 39.3%; Score 46; DB 2; Length 1609;  
Best Local Similarity 66.7%; Pred. NO. 1e+02;  
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 ILEGRTECVLSN 16  
:|||||:|:|:  
DB 877 LLEGRTECVWSS 888  
  
RESULT 12  
S42639  
ATP-dependent RNA helicase DB10 - wood tobacco  
C:Species: Nicotiana sylvestris (wood tobacco)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 19-Jan-2001  
C:Accession: S42639  
R:Itadani, H.; Sugita, M.; Sugiura, M.  
Plant Mol. Biol. 24, 249-252, 1994  
A:Title: Structure and expression of a cDNA encoding an RNA helicase-like protein in tot  
A:Reference number: S42639; MUID:94154240; PMID:8111024  
A:Accession: S42639  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-607 <ITA>  
A:Cross-references: GB:D16247; NID:9466572; PIDN:BA03763.1; PID:9563986  
C:Superfamily: tobacco ATP-dependent RNA helicase DB10; WW repeat homology  
C:Keywords: ATP; nucleotide binding; P-loop  
P:18-56/Domain: WW repeat homology <WW1>  
P:189-196/Region: nucleotide-binding motif A (P-loop)  
P:294-299/Region: nucleotide-binding motif B  
P:298-301/Region: DEAD motif  
  
Query Match 38.9%; Score 45.5; DB 1; Length 607;  
Best Local Similarity 37.9%; Pred. NO. 44;  
Matches 11; Conservative 4; Mismatches 5; Indels 9; Gaps 1;  
  
QY 3 VEILEGRTECVLSNLR-----GRTR 22  
:|||||:|:|:  
DB 505 VKVLEGANQCVTELRDMASRGGMGRAR 533  
  
RESULT 13  
D83406  
probable transmembrane sensor PA1911 [imported] - Pseudomonas aeruginosa (strain PA01)  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 28-Jul-2003  
C:Accession: D83406  
R:Stover, C.K.; Yam, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
A:Reference number: AB2950; MUID:20437337; PMID:10984043  
A:Accession: D83406  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-316 <STO>  
A:Cross-references: GB:AE004617; GB:AE004091; NID:99947901; PIDN:AAG05299.1; GSPDB:GN001  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA1911  
C:Superfamily: Fe2+-dicitrate sensor, transmembrane component  
  
Query Match 38.5%; Score 45; DB 2; Length 316;  
Best Local Similarity 54.5%; Pred. NO. 27;  
Matches 12; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

```
7; Indels 0; Gaps 0;
```

7 EGRTECVLSNLRGRTRY 23  
296 EGTYECEAEINIKGRDITY 312

Search completed: May 6, 2004, 12:47:27  
Job time : 22 secs

QY            2 RVEILLEGRTCVLSNLRGTRY 23  
       || | || | | | | | :  
Db          195 RVAVLAGRVE--LSPHGRGW 214

RESULT 14

D70506  
hypothetical protein RV2733c - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000  
C:Accession: D70506  
Rv2733c, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A:A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295987; PMID:9634230  
A:Accession: D70506  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-512 <COL>  
A:Cross-references: GB:Z98209; GB:AL123456; PIDN:CAB10909.1; PID:g2292967  
A:Experimental source: strain H37RV  
C:GeneticS:  
A:Gene: RV2733c  
C:Superfamily: conserved hypothetical protein b0835

Query Match 38.5%; Score 45; DB 1; Length 512;  
Best Local Similarity 42.3%; Pred. No. 44;  
Matches 11; Conservative 4; Mismatches 7; Indels 4; Gaps 1;

```

Qy      1 QRV EIL-----EGRTCTVLSNLRGTR 22
          ||| : | : | : |
Db      408 QAVEVLVATGEGRKDTVTARMSGRAR 433

RESULT 15
axonin-1 precursor - chicken
N:Alternate names: neural cell adhesion molecule AxCAM
C:Species: Gallus gallus (Chicken)
C>Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: S22383; S34107; S69332; S22128
R:Zuellig, R.A.; Rader, C.; Schroeder, A.; Kalousek, M.B.; von Bohlen und Halbach, F.; O
Eur. J. Biochem. 204, 453-463, 1992
A:A>Title: The axonally secreted cell adhesion molecule, axonin-1. Primary structure, immu
A:Reference number: S22383; MUID:92174898; PMID:1311675
A:Accession: S22383
A:Molecule type: mRNA
A:Residues: 1-1036 <ZU81>
A:Cross-references: EMBL:X63101; NID:G62852; PIDN:CAA44815.1; PID:G62853
A:Accession: S34107
A:Molecule type: protein
A:Residues: 29-49;51-80;84-95;100-117;120-128;130-141;143-176;243-254;256-296;303-336;33
R:Rigler, R.J.; Vogt, L.; Zuellig, R.A.; Rader, C.; Henahan-Beatty, A.; Wolfer, D.P.; Son
Eur. J. Biochem. 227, 617-628, 1995
A:A>Title: The gene of chicken axonin-1. Complete structure and analysis of the promoter.
A:Reference number: S69332; MUID:95172044; PMID:7867620

```

A.Accession: S85322  
A.Status: preliminary; nucleic acid sequence not shown; translation not shown  
A.Molecule type: DNA  
A.Residues: 1002-1036 <GIG>  
A.Cross-references: EMBL:X79607  
A.Note: The nucleotide sequence was submitted to the EMBL Data Library, June 1994  
C.Superfamily: contactin; fibronectin type III repeat homology; immunoglobulin homology  
C.Keywords: cell adhesion  
P.1-23/Domains: signal sequence #status predicted <SIG>  
P.24-1036/Product: axonin 1 #status predicted <MAT>  
P.336-392/Domains: immunoglobulin homology <IMM>

Query Match

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 6, 2004, 12:38:56 ; Search time 54 Seconds  
(without alignments)  
120.344 Million cell updates/sec

Title: US-10-612-885A-1

Perfect score: 117

Sequence: 1 ORVEILEGRTECVLSNLRGTRY 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Genesecp\_29Jan04:\*

1: Genesecp1980s:\*

2: Genesecp1990s:\*

3: Genesecp2000s:\*

4: Genesecp2001s:\*

5: Genesecp2002s:\*

6: Genesecp2003as:\*

7: Genesecp2003bs:\*

8: Genesecp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	117	100.0	23	2 AAY39411	Aay39411 Human ery
2	117	100.0	23	5 AAU78011	Aau78011 Human ery
3	117	100.0	23	6 ABP72837	Abp72837 Erythro
4	117	100.0	30	2 AAR98938	Aar98938 Synthetic
5	117	100.0	211	3 AAB21686	Aab21686 Human mat
6	117	100.0	225	3 AAB21685	Aab21685 Human mat
7	117	100.0	438	3 AAY44622	Aay44622 Truncated
8	117	100.0	438	3 AAY44623	Aay44623 R154C tru
9	117	100.0	458	7 ADE28671	Ade28671 Human NOV
10	117	100.0	458	7 ADE28673	Ade28673 Human NOV
11	117	100.0	458	7 ADE28675	Ade28675 Human NOV
12	117	100.0	488	2 AAW08349	Aaw08349 EpoRfc fu
13	117	100.0	503	3 AAB13012	Aab13012 Q-tagged
14	117	100.0	508	2 AAR06512	Aar06512 EPO recep
15	117	100.0	508	2 AAR47518	Aar47518 Human EPO
16	117	100.0	508	2 AAR70032	Aar70032 Human ery
17	117	100.0	508	2 AAR69503	Aar69503 Human ery
18	117	100.0	508	5 ABB09173	Abb09173 Human ery
19	111	94.9	508	7 ADE28677	Ade28677 Human NOV
20	109	93.2	285	2 AAR50326	Aar50326 Mouse sol
21	109	93.2	507	2 AAR06511	Aar06511 EPO recep
22	109	93.2	507	2 AAR47517	Aar47517 MEL EPO r
23	109	93.2	507	2 AAR69502	Aar69502 Mouse ery
24	102	87.2	507	2 AAR50327	Aar50327 Mouse sol
25	54	44.4	1026	5 AAU80379	Aau80379 Human BIG

#### ALIGNMENTS

RESULT 1

AAV39411

ID AAY39411 standard; peptide; 23 AA.

XX AC AAY39411;

XX XX 30-NOV-1999 (first entry)

XX DE Human erythropoietin receptor-derived activation peptide.

XX KW Erythropoietin; EPO; receptor; activation; internalisation.

XX OS Synthetic.

OS OS Homo sapiens.

XX FN WO9942127-A2.

XX PD 26-AUG-1999.

XX PF 23-FEB-1999; 99WO-US003910.

XX PR 24-FEB-1998; 98US-00028938.

XX (RECE-) RECEPTRON INC.

PA Olsson L, Naranda T;

XX WPI; 1999-527422/44.

XX PT Modulating activity of type-2 cell surface receptors used in treatment of, e.g. obesity.

XX PS Claim 8; Page 17; 92pp; English.

XX This sequence represents a peptide derived from the extracellular activation sequence of the human erythropoietin (EPO) receptor.  
CC Activation sequences are involved in modulation of receptor responses and are separate from the ligand binding site. Activation sequences are important in two distinct ways: in the modulation of receptor internalisation; and/or in the modulation of activation of the receptor. Use of peptides corresponding to the activation sequence of a receptor can retard or inhibit receptor internalisation, thereby increasing or stabilising the steady-state number of active receptors on the cell surface. This has the effect of increasing signalling per unit of ligand. In addition, the receptor is classed as a type 2 cell surface receptor, meaning that such peptides can actually replace the requirement for the ligand, causing ligand-independent activation. This activation is probably brought about by a dimerisation mechanism in which one peptide

CC molecule is bound by two receptors, mimicking the dimerisation and  
CC subsequent activation that occurs when two receptors bind one ligand.  
CC This peptide could be used to treat disorders involving an inadequate or  
CC inappropriate response from its corresponding receptor

XX SQ Sequence 23 AA;  
SQ Query Match 100.0%; Score 117; DB 2; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3.6e-11; Indels 0; Gaps 0;  
Matches 23; Conservative 0; Mismatches 0

QY 1 QRVLEIGRTECVLSNLRGRTRY 23  
Db 1 QRVLEIGRTECVLSNLRGRTRY 23

RESULT 2  
AAU78011  
ID AAU78011 standard; peptide; 23 AA.  
XX AAU78011  
AC AAU78011  
XX 05-JUN-2002 (first entry)  
XX Human erythropoietin receptor activation domain oligopeptide.  
XX Erythropoietin receptor; antidiabetic; activation sequence; ligand;  
KW receptor internalisation; type 2 diabetes; drug screening; human.  
XX Homo sapiens.  
XX US6333031-B1.  
PN 25-DEC-2001.  
PD 24-FEB-1998; 98US-00028937.  
XX 08-MAR-1996; 96US-00612999.  
PR 22-AUG-1996; 96US-00701382.  
PR 23-JAN-1997; 97US-00788820.  
XX (RECE-) RECEPTRON INC.  
XX Olsson L; Naranda T;  
XX WPI; 2003-224899/28.  
XX Composition comprising peptides from receptor extracellular domains,  
PT useful for e.g. modulating receptor internalization and activation such  
PT as increasing insulin activity.  
XX Claim 1; Col 11; 48pp; English.  
XX This invention corresponds to a novel composition comprising any of 34  
CC peptides consisting of activation sequences from the extracellular  
CC domains of cell-surface receptors. These peptides were identified by  
CC homology searching with a peptide sequence from the MHC class I alpha I  
CC domain and correspond to the activation sequences of the associated  
CC receptor. Activation sequences are involved in the internalisation of  
CC receptors and so these peptides may be used to modulate the  
CC internalisation and or activation of these receptors. The peptides of the  
CC invention may also be used to increase effect of ligand signalling in  
CC type 2 diabetes and can replace the ligand normally required for  
CC activation. This is useful when the ligand is a hormone and is difficult  
CC to obtain. The peptides may also interact synergistically with the ligand  
CC or function as antagonists of receptor signalling. The peptides can also  
CC be used in drug screening to identify compounds that modulate receptor  
CC internalisation or function as ligand replacements. Use of these peptides  
CC can increase the effect of therapeutic hormones (optionally co-  
CC administered) by at least 50% and are specific for the receptors from  
CC which they derive. The present sequence represents the human  
CC Erythropoietin receptor activation sequence oligopeptide of the invention  
XX

SQ Sequence 23 AA;  
SQ Query Match 100.0%; Score 117; DB 5; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3.6e-11; Indels 0; Gaps 0;  
Matches 23; Conservative 0; Mismatches 0

QY 1 QRVLEIGRTECVLSNLRGRTRY 23  
Db 1 QRVLEIGRTECVLSNLRGRTRY 23

RESULT 3  
ABP72837  
ID ABP72837 standard; peptide; 23 AA.  
XX ABP72837;  
AC ABP72837;  
XX 11-AUG-2003 (first entry)  
XX Erythropoietin mimetic peptide.  
XX Transferin; neuroprotective; cerebroprotective; vasotropic;  
KW antiparkinsonian; nootropic; anti-HIV; antiasthmatic; anti-allergic;  
KW cytostatic; immunosuppressive; antithrombotic; cardiant;  
KW gynaecological; immunostimulant; antianaemic; haemostatic;  
KW antiinflammatory; dermatological; antibacterial; virucide; antiparasitic;  
KW fungicide; hepatotropic; antirheumatic; antiarthritic; antigout;  
KW tranquilizer; vulnerary; antidiabetic; nephrotropic; antipyretic;  
KW gastrointestinal; gene therapy; transgenic animal; erythropoietin;  
KW mimetic; agonist.  
XX Synthetic.  
OS WO2003020746-A1.  
XX 13-MAR-2003.  
XX 30-AUG-2002; 2002WO-US027637.  
XX 30-AUG-2001; 2001US-0315745P.  
PR 30-NOV-2001; 2001US-0334059P.  
XX (BIOR-) BIOREXIS PHARM CORP.  
XX Prior CP;  
XX WPI; 2003-332916/31.  
XX New fusion protein, useful in the diagnosis and treatment of diseases or  
PT disorders relating to the respiratory, cardiovascular and digestive  
PT systems, comprises a transferrin protein fused to a therapeutic protein.  
XX Example 9; Page 255; 298pp; English.  
XX The present sequence is that of an erythropoietin (EPO) mimetic peptide  
CC which has no homology to natural EPO but has similar biological  
CC properties in that it activates the EPO receptor acting as an agonist.  
CC The EPO mimetic peptide can be included in novel fusion proteins of the  
CC invention also including a transferrin (Tf, see ABP72820) moiety  
CC engineered to extend the serum half-life or bioavailability. The EPO  
CC mimetic peptide can be fused to the N- or C-terminus of Tf, or inserted  
CC into, or used to replace part of Tf, such that the Tf acquires EPO  
CC activity. Modified Tf fusion proteins of the invention can be used in the  
CC diagnosis, prognosis, prevention and/or treatment of diseases and/or  
CC disorders of the endocrine, nervous, immune, respiratory, cardiovascular,  
CC reproductive and digestive systems, diseases and/or disorders relating to  
CC the blood or to cell proliferation, inflammatory conditions and  
CC infectious diseases, or to deliver a therapeutic agent to a cell or  
CC across the blood-brain barrier  
XX SQ Sequence 23 AA;  
SQ Query Match 100.0%; Score 117; DB 6; Length 23;



```
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ORVEILGRTCEVLNLGRTRY 23
DB 1 ORVEILGRTCEVLNLGRTRY 23

RESULT 4
AAR98938
ID AAR98938 standard; peptide; 30 AA.
XX AC AAR98938
XX DT 28-SEP-1996 (first entry)
XX DE Synthetic human erythropoietin receptor peptide, SE-8.
XX KW Monoclonal antibody; erythropoietin receptor; diagnosis; anaemia;
XX OS erythropoiesis; erythrocyte production; epitope mapping.
XX PN Synthetic.
XX PD WO9603438-A1.
XX PP 08-FEB-1996.
XX PR 26-JUL-1995; 95WO-US009458.
XX PA 26-JUL-1994; 94US-00280864.
XX PI (AMGE-) AMGEN INC.
XX PT Elliott SG;
XX DR WPI; 1996-117004/12.
XX PT Monoclonal antibodies stimulating an erythropoietin receptor - useful in
XX PT diagnosis and treatment of patients having disorders associated with low
XX PT red blood cell levels, e.g. anaemia.
XX PS Example 6; Page 34; 61pp; English.
XX CC AAR89960-R89965 and AAR98936-R98939 are overlapping, synthetic human
XX CC erythropoietin receptor (shEPO) peptides which span residues 1 to 244
XX CC of the human EPOR. The peptides are used to map the EPOR binding epitope
XX CC of an EPOR monoclonal antibody which binds to EPORs and stimulates
XX CC erythropoiesis by stimulating the proliferation and/or differentiation of
XX CC erythroid progenitor cells to erythrocytes. Pharmaceutical compans.
XX CC contg. the antibody may be used in the diagnosis and treatment of
XX CC patients having disorders associated with low red blood cell levels, e.g.
XX CC anaemia. The antibodies are also useful in methods and kits for detecting
XX CC EPORs in biological in biological samples
XX SQ Sequence 30 AA;

Query Match 100.0%; Score 117; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.9e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ORVEILGRTCEVLNLGRTRY 23
DB 1 ORVEILGRTCEVLNLGRTRY 23

RESULT 5
AAB21686
ID AAB21686 standard; peptide; 211 AA.
XX AC AAB21686;
XX DT 21-DEC-2000 (first entry)
XX PA (XENC-) XENCOR INC.
XX XX

Human mature erythropoietin receptor EPOR extracellular domain #2.
Ligand; cell surface receptor; erythropoietin; EPOR; human;
protein design automation; PDA.
Homo sapiens.
WO2000047612-A2.
17-AUG-2000.
11-FEB-2000; 2000WO-US003665.
11-FEB-1999; 99US-0120009P.
29-APR-1999; 99US-0131674P.
(XENC-) XENCOR INC.
Luo P, Dahlyat B;
WPI; 2000-549135/50.
Screening for ligand analogs and agents which modulate ligand-receptor
binding, comprises adding a test ligand to a non-naturally occurring cell
surface receptor analog.
Example 1; Fig 8; 82pp; English.
The present invention relates to a method for screening for a ligand
analog, comprising adding a candidate ligand to a non-naturally occurring
cell surface receptor analog e.g. erythropoietin receptor (EPOR), and
determining the binding of the ligand to the analog. The present sequence
is a mature human erythropoietin receptor (EPOR) extracellular domain.
Protein Design Automation was carried out on the present sequence, so
that it may be used in the present invention as a cell surface receptor
analog
Sequence 211 AA;
Query Match 100.0%; Score 117; DB 3; Length 211;
Best Local Similarity 100.0%; Pred. No. 4.7e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ORVEILGRTCEVLNLGRTRY 23
DB 161 ORVEILGRTCEVLNLGRTRY 183

RESULT 6
AAB21685
ID AAB21685 standard; peptide; 225 AA.
XX AC AAB21685;
XX DT 21-DEC-2000 (first entry)
XX DE Human mature erythropoietin receptor EPOR extracellular domain #1.
XX KW Ligand; cell surface receptor; erythropoietin; EPOR; human.
XX OS Homo sapiens.
XX PN WO2000047612-A2.
XX PD 17-AUG-2000.
XX PR 11-FEB-2000; 2000WO-US003665.
XX PR 11-FEB-1999; 99US-0120009P.
XX PR 29-APR-1999; 99US-0131674P.
XX PA (XENC-) XENCOR INC.
XX XX
```

```
PI Luo P, Bahiyat B;
XX WPI; 2000-549135/50.
XX
XX Screening for ligand analogs and agents which modulate ligand-receptor
PT binding, comprises adding a test ligand to a non-naturally occurring cell
PT surface receptor analog.
XX
XX Example 1; Fig 8; 82pp; English.
XX
XX The present invention relates to a method for screening for a ligand
XX analog, comprising adding a candidate ligand to a non-naturally occurring
XX cell surface receptor analog e.g. erythropoietin receptor (EPoR), and
XX determining the binding of the ligand to the analog. The present sequence
XX is a mature human erythropoietin receptor (EPoR) extracellular domain.
XX This sequence may be used in the present invention as a cell surface
XX receptor analog.
XX
XX Sequence 225 AA;
SQ
Query Match 100.0%; Score 117; DB 3; Length 225;
Best Local Similarity 100.0%; Pred. No. 5e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QRVILEGRTECVLSNLRGTRY 23
DB 170 QRVILEGRTECVLSNLRGTRY 192
RESULT 7
AAY44622
ID AAY44622 standard; protein; 438 AA.
XX
XX AC AAY44622;
XX
XX DT 07-APR-2000 (first entry)
XX
XX DE Truncated human EpOR(t439).
XX
XX KW Truncated human EpOR; erythropoietin receptor; hypersensitive EpOR(t439);
XX mutant human EpOR; EpOR signalling; cancer; infectious disease; HIV;
XX sickle cell anaemia; cytostatic; antimicrobial; antiviral;
XX immunostimulant; anti-anaemic.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 154
XX FT /note= "Wild type Arg substituted by Cys"
XX
XX FN WO9967360-A2.
XX
XX PN 29-DEC-1999.
XX
XX PD 25-JUN-1999; 99WO-CA000606.
XX
XX PF Truncated human EpOR; erythropoietin receptor; hypersensitive EpOR(t439);
XX mutant human EpOR; EpOR signalling; cancer; infectious disease; HIV;
XX sickle cell anaemia; cytostatic; antimicrobial; antiviral;
XX immunostimulant; anti-anaemic.
XX
XX PA (HEMO-) HEMOSOL INC.
XX
XX OS Homo sapiens.
XX
XX PN WO9967360-A2.
XX
XX PD 29-DEC-1999.
XX
XX PF 25-JUN-1999; 99WO-CA000606.
XX
XX PR 25-JUN-1998; 98CA-02241576.
XX
XX PR 25-JAN-1999; 99CA-02260332.
XX
XX PA (HEMO-) HEMOSOL INC.
XX
XX PI Bell D, Matthews KE, Mueller SG;
XX
XX WPI; 2000-136979/12.
XX
XX PD P-PSDB; AAZ49634.
XX
XX PF Serum free defined medium useful for the efficient culture of stem cells
XX used for production of hemoglobin.
XX
XX PS Example 6; Fig 9; 61pp; English.
XX
XX CC The present sequence is truncated human EpOR (erythropoietin receptor).
XX Transfection of constitutively active EpOR(t439) by electroporation into
XX a cytokine-dependent cell line supports cell population expansion in the
XX absence of exogenous cytokines. Mutant human EpOR is used in treatment of
XX disorders related to inadequate EpOR signalling. The transfected cells
XX may also used in gene therapy to treat cancer, infectious diseases (e.g.
XX HIV), sickle cell anaemia, and conditions related to abnormal expression
XX of erythropoietin
XX
XX CC Query Match 100.0%; Score 117; DB 3; Length 438;
XX Best Local Similarity 100.0%; Pred. No. 1.1e-09;
XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 QRVILEGRTECVLSNLRGTRY 23
XX DB 194 QRVILEGRTECVLSNLRGTRY 216
RESULT 8
AAY44623
ID AAY44623 standard; protein; 438 AA.
XX
XX AC AAY44623;
XX
XX DT 07-APR-2000 (first entry)
XX
XX DE R154C truncated human EpOR(t439).
XX
XX KW Truncated human EpOR; erythropoietin receptor; hypersensitive EpOR(t439);
XX mutant human EpOR; EpOR signalling; cancer; infectious disease; HIV;
XX sickle cell anaemia; cytostatic; antimicrobial; antiviral;
XX immunostimulant; anti-anaemic.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 154
XX FT /note= "Wild type Arg substituted by Cys"
XX
XX FN WO9967360-A2.
XX
XX PN 29-DEC-1999.
XX
XX PD 25-JUN-1999; 99WO-CA000606.
XX
XX PF Truncated human EpOR; erythropoietin receptor; hypersensitive EpOR(t439);
XX mutant human EpOR; EpOR signalling; cancer; infectious disease; HIV;
XX sickle cell anaemia; cytostatic; antimicrobial; antiviral;
XX immunostimulant; anti-anaemic.
XX
XX PA (HEMO-) HEMOSOL INC.
XX
XX OS Homo sapiens.
XX
XX PI Bell D, Matthews KE, Mueller SG;
XX
XX WPI; 2000-136979/12.
XX
XX PD N-PSDB; AAZ49636.
XX
XX PF Serum free defined medium useful for the efficient culture of stem cells
XX used for production of hemoglobin.
XX
XX PS Example 6; Fig 10; 61pp; English.
XX
XX CC The present sequence is R154C truncated human EpOR (erythropoietin
XX receptor). Transfection of constitutively active EpOR(t439; R154C) by
XX electroporation into a cytokine-dependent cell line supports cell
XX population expansion in the absence of exogenous cytokines. Mutant human
XX EpOR is used in treatment of disorders related to inadequate EpOR
XX signalling. The transfected cells may also used in gene therapy to treat
XX cancer, infectious diseases (e.g. HIV), sickle cell anaemia, and
XX conditions related to abnormal expression of erythropoietin
XX
XX CC Query Match 100.0%; Score 117; DB 3; Length 438;
XX Best Local Similarity 100.0%; Pred. No. 1.1e-09;
XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 QRVILEGRTECVLSNLRGTRY 23
XX DB 194 QRVILEGRTECVLSNLRGTRY 216
```

Db 194 QRVLEGRTECVLSNLRGTRY 216

RESULT 9

ADE28671

ID ADE28671 standard; protein; 458 AA.

AC ADE28671;

XX

DT 29-JAN-2004 (first entry)

XX

DE Human NOV15a protein - SEQ ID 48.

XX

XX NOX; antidiabetic; anorectic; cardiatic; hypotensive;

KW antiarteriosclerotic; virucide; antibacterial; fungicide; protozoacide;

KW neurotropic; neuroprotective; antiparkinsonian; anticonvulsant;

KW osteopathic; antiarthritic; antiinflammatory; dermatological;

KW anorexia; cancer; cardiovascular; hypertensive; diabetes; obesity; infectious;

KW neurodegenerative; Alzheimer's disease; Parkinson's; epilepsy; immune;

KW osteoarthritis; haemopoietic; inflammatory skin; asthma; dyslipidaemia;

KW neurogenesis; cell differentiation; proliferation; haemopoiesis;

KW wound healing; angiogenesis; gene therapy; chromosome mapping;

KW tissue typing; human; NOV.

XX

OS Homo sapiens.

XX

PN W02003040330-A2.

XX

PD 15-MAY-2003.

XX

PF 05-NOV-2002; 2002WO-US035536.

XX

PR 05-NOV-2001; 2001US-0338626P.

PR 05-DEC-2001; 2001US-0336600P.

PR 07-DEC-2001; 2001US-0338285P.

PR 12-DEC-2001; 2001US-0341346P.

PR 17-DEC-2001; 2001US-0341477P.

PR 20-DEC-2001; 2001US-0342592P.

PR 27-DEC-2001; 2001US-0344297P.

PR 31-OCT-2002; 2002US-00287971.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Alvarez E, Anderson DW, Baron M, Boldog FL;

PI Burgess CE, Casman SJ, Chapoval A, Dhanabal M, Edinger SR, Eisen A;

PI Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L;

PI Grosse WM, Guo X, Hackett C, Ji W, Kekuda R, Khramtsov NV;

PI Lepley DM, Li L, Macdougall JR, Malyankar UM, Mazur A, Mcqueeney K;

PI Mezes PS, Miller CB, Millet I, Mishra VS, Padigaru M, Patturajan M;

PI Pena CEA, Peyman JA, Rastelli L, Rieger DK, Shenoy SG, Shimkets RA;

PI Smithson G, Starling G, Spytek KA, Stone DJ, Tchernev VT, Twonlow N;

PI Vernet CAM, Zerhusen BD, Zhong M;

XX

XX WPI; 2003-441555/41.

XX N-PSDS; ADE28670.

DR

XX

PT New isolated NOX polypeptides and polynucleotides, useful for

PT preventing, diagnosing or treating NOX-associated disorders, e.g.

PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,

PT asthma, or infections.

XX

PS Claim 1; SEQ ID NO 48; 447pp; English.

XX

CC The invention relates to a novel isolated NOX polypeptide. The

CC polypeptide of the invention demonstrates, antidiabetic, anorectic,

CC cardiatic, hypotensive, antiarteriosclerotic, virucide, antibacterial,

CC fungicide, protozoacide, neurotropic, neuroprotective, antiparkinsonian,

CC anticonvulsant, osteopathic, antiarthritic, antiinflammatory,

CC dermatological, antiasthmatic and antilipemic activities. The

CC polypeptides, nucleic acid molecules and antibodies may be useful for

CC treating or diagnosing diseases including metabolic disorders such as

CC diabetes and obesity, infectious diseases, anorexia, cancer,

CC cardiovascular diseases including hypertension and atherosclerosis,

CC neurodegenerative disorders such as Alzheimer's disease, Parkinson's

CC disease and epilepsy, immune disorders e.g. osteoarthritis, haemopoietic

CC disorders, inflammatory skin disorders, asthma and dyslipidaemia.

CC Furthermore, the nucleic acids and polypeptides may also be used to

CC identify molecules that modulate or inhibit neurogenesis, cell

CC differentiation and proliferation, haemopoiesis, wound healing and

CC angiogenesis, as well as in gene therapy. Finally, the nucleic acids may

CC be used as hybridisation probes, in chromosome mapping, tissue typing,

CC preventive medicine and pharmacogenomics. The current sequence is that of

CC the human NOV protein of the invention.

XX

XX Sequence 458 AA;

Qy 1 QRVLEGRTECVLSNLRGTRY 23

Db 194 QRVLEGRTECVLSNLRGTRY 216

RESULT 10

ADE28673

ID ADE28673 standard; protein; 458 AA.

XX

AC ADE28673;

XX

DT 29-JAN-2004 (first entry)

XX

DE Human NOV15b protein - SEQ ID 50.

XX

XX NOX; antidiabetic; anorectic; cardiatic; hypotensive;

KW antiarteriosclerotic; virucide; antibacterial; fungicide; protozoacide;

KW neurotropic; neuroprotective; antiparkinsonian; anticonvulsant;

KW osteopathic; antiarthritic; antiinflammatory; dermatological;

KW anorexia; cancer; cardiovascular; hypertensive; diabetes; obesity; infectious;

KW neurodegenerative; Alzheimer's disease; Parkinson's; epilepsy; immune;

KW osteoarthritis; haemopoietic; inflammatory skin; asthma; dyslipidaemia;

KW neurogenesis; cell differentiation; proliferation; haemopoiesis;

KW wound healing; angiogenesis; gene therapy; chromosome mapping;

KW tissue typing; human; NOV.

XX

OS Homo sapiens.

XX

PN W02003040330-A2.

XX

PD 15-MAY-2003.

XX

PF 05-NOV-2002; 2002WO-US035536.

XX

PR 05-NOV-2001; 2001US-0338626P.

PR 05-DEC-2001; 2001US-0336600P.

PR 07-DEC-2001; 2001US-0338285P.

PR 12-DEC-2001; 2001US-0341346P.

PR 17-DEC-2001; 2001US-0341477P.

PR 20-DEC-2001; 2001US-0342592P.

PR 27-DEC-2001; 2001US-0344297P.

PR 31-OCT-2002; 2002US-00287971.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Alvarez E, Anderson DW, Baron M, Boldog FL;

PI Burgess CE, Casman SJ, Chapoval A, Dhanabal M, Edinger SR, Eisen A;

PI Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L;

PI Grosse WM, Guo X, Hackett C, Ji W, Kekuda R, Khramtsov NV;

PI Lepley DM, Li L, Macdougall JR, Malyankar UM, Mazur A, Mcqueeney K;

PI Mezes PS, Miller CB, Millet I, Mishra VS, Padigaru M, Patturajan M;

PI Pena CEA, Peyman JA, Rastelli L, Rieger DK, Shenoy SG, Shimkets RA;

PI Smithson G, Starling G, Spytek KA, Stone DJ, Tchernev VT, Twonlow N;

PI Vernet CAM, Zerhusen BD, Zhong M;

XX

XX WPI; 2003-441555/41.

XX N-PSDS; ADE28670.

DR

XX

PT New isolated NOX polypeptides and polynucleotides, useful for

PT preventing, diagnosing or treating NOX-associated disorders, e.g.

PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,

PT asthma, or infections.

XX

Query Match 100.0%; Score 117; DB 7; Length 458;

Best Local Similarity 100.0%; Pred. No. 1.1e-09;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



CC cardiovascular diseases including hypertension and atherosclerosis,  
CC neurodegenerative disorders such as Alzheimer's disease, Parkinson's  
CC disease and epilepsy, immune disorders e.g. osteoarthritis, haemopoietic  
CC disorders, inflammatory skin disorders, asthma and dyslipidaemia.  
CC Furthermore, the nucleic acids and polypeptides may also be used to  
CC identify molecules that modulate or inhibit neurogenesis, cell  
CC differentiation and proliferation, haemopoiesis, wound healing and  
CC angiogenesis, as well as in gene therapy. Finally, the nucleic acids may  
CC be used as hybridisation probes, in chromosome mapping, tissue typing,  
CC preventive medicine and pharmacogenomics. The current sequence is that of  
CC the human NOV protein of the invention.

XX Sequence 458 AA;

Query Match 100.0%; Score 117; DB 7; Length 458;  
Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRVLEIGRTECVLSNLRGTRY 23  
Db 194 QRVLEIGRTECVLSNLRGTRY 216

RESULT 12  
AAW08349  
ID AAW08349 standard; protein; 488 AA.  
XX  
AC AAW08349;  
DT 14-MAR-1997 (first entry)  
XX  
DE EpoRfc fusion protein.  
XX  
KW Receptor agonist; antibody; erythropoietin receptor; EpoR; immunogen;  
KW antigen; metallothionein; promoter; IGGI; Fc; anaemia; therapy.  
XX  
OS Homo; sapiens.  
OS Synthetic.  
OS Chimeric.  
XX  
PH Key Location/Qualifiers  
FT Domain 1. .250  
FT /label= EpoR-ECD  
FT /note= "erythropoietin receptor extracellular domain"  
FT Cleavage-site 251. .254  
FT /note= "Factor Xa cleavage site"  
FT Domain 255. .488  
FT /label= Fc  
FT /note= "human IgG1 Fc sequence"  
XX  
XX WO9640231-A1.  
XX  
XX 19-DEC-1996.  
XX  
XX 07-JUN-1996; 96WO-US009613.  
XX  
XX 07-JUN-1995; 95US-00474673.  
XX  
XX (SMIK ) SMITHKLINE BEECHAM CORP.  
XX  
XX Young PR, Erickson-Miller CL;  
XX  
XX WPI; 1997-051900/05.  
XX  
XX N-PSDB; AAT48800.  
XX  
XX Recombinant immunogen corresp. to dimeric form of a receptor - used for  
XX generating antibodies able to act as receptor agonists, esp. of  
XX erythropoietin receptor for treating anaemia.  
XX  
XX Example 1; Page 39-41; 83pp; English.  
XX  
XX A fusion protein (AAW08349) encoded by plasmid mtaIsEpoRfc (AAT48800)  
CC comprises the human erythropoietin receptor (EpoR) extracellular domain

CC fused (via a Factor Xa cleavage sequence) to the Fc portion of human  
CC IgG1. It can be expressed e.g. in transfected Drosophila S2 cells upon  
CC induction with copper sulphate. The cells secrete EpoRfc as a dimeric  
CC molecule due to the affinity of the Fc moiety for itself. The dimeric  
CC receptor can be used as an immunogen to generate antibodies (monoclonal,  
CC polyclonal, chimeric, humanised) able to act as EpoR agonists for use in  
CC treatment of anaemia

XX Sequence 488 AA;

Query Match 100.0%; Score 117; DB 2; Length 488;  
Best Local Similarity 100.0%; Pred. No. 1.2e-09;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRVLEIGRTECVLSNLRGTRY 23  
Db 194 QRVLEIGRTECVLSNLRGTRY 216

RESULT 13  
AAB13012  
ID AAB13012 standard; protein; 503 AA.  
XX  
AC AAB13012;  
XX  
DT 08-DEC-2000 (first entry)  
XX  
DE Q-tagged erythropoietin (EPO) receptor protein.  
XX  
KW Site specific label; detection; interaction screening; transglutaminase;  
KW erythropoietin receptor; EPO.  
XX  
OS Synthetic.  
XX  
XX WO200043492-A2.  
XX  
XX 27-JUL-2000.  
XX  
XX 20-JAN-2000; 2000WO-US001481.  
XX  
XX 22-JAN-1999; 99US-0117327P.  
XX  
XX (SMIK ) SMITHKLINE BEECHAM CORP.  
XX  
XX Tew DG, Powell DJ, Meek TD, Chen W;  
XX  
XX WPI; 2000-499222/44.

Screening for a candidate compound for use in bioassays comprises  
contacting the candidate molecule with a labelled modified protein and  
detecting the label to identify interaction of the two molecules.

Example 4; Page 26; 49pp; English.

This invention relates to methods for the site specific modification of a  
protein, and to a method for screening for a candidate compound which  
interacts with first protein. The screening method comprises contacting  
the candidate molecule with a labelled modified first protein and  
detecting the label to identify interaction of the labelled modified  
first protein and candidate compound. The first protein is modified to  
contain a peptide, represented by sequence AAB13005. The method is used  
to label proteins at specific sites. The present sequence represents a Q-  
tagged erythropoietin (EPO) receptor constructed in an example of the  
method of the invention

XX Sequence 503 AA;

Query Match 100.0%; Score 117; DB 3; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.3e-09;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRVLEIGRTECVLSNLRGTRY 23  
Db 194 QRVLEIGRTECVLSNLRGTRY 216

Db 194 ORVEILGRTCVLSNLRGTRY 216

RESULT 14  
AAR06512 standard; protein; 508 AA.

XX AAR06512  
AC AAR06512  
DT 25-MAR-2003 (revised)  
DT 04-JAN-1991 (first entry)  
XX  
DE EPO receptor.  
XX  
XX Erythropoietin; Diamond Blackfan anaemia; polycythemia vera.  
KW  
XX  
XX Homo sapiens.  
OS  
FN W09008822-A.  
XX  
XX 09-AUG-1990.  
PD  
XX  
XX 03-FEB-1989; 89US-00306503.  
PF  
XX  
XX 03-FEB-1989; 89US-00306503.  
PR  
XX  
XX (GEM) GENETICS INST INC.  
PA  
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.  
XX  
XX Dandrea A, Wong G;  
PI  
XX  
XX WPI; 1990-260931/34.  
DR  
DR N-PSDB; AAQ05748.  
XX  
XX Erythropoietin receptor and gene - used for developing reagents and  
PT systems to control and study erythropoiesis.  
PT  
XX  
XX Disclosure; Fig 2; 53pp; English.  
PS  
XX  
XX The sequence was deduced from DNA obtd. from a clone isolated from a  
CC commercially available human genomic cDNA library in phage Lambda Fix  
CC (Stratagene). The sequence encodes a type I trans- membrane protein with  
CC binding affinity for EPO. The gene and recombinant EPO receptor produced  
CC on expression of the DNA are used to develop reagents and systems to  
CC control and study erythropoiesis. It is believed that the EPO receptor is  
CC dys- functional in individuals with Diamond Blackfan anaemia, and may be  
CC hyperactive in polycythemia vera. See also AAR06511 (murine EPO  
CC receptor). (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-  
CC MAR-2003 to correct PI field.)  
XX  
XX Sequence 508 AA;

Query Match 100.0%; Score 117; DB 2; Length 508;  
Best Local Similarity 100.0%; Pred. No. 1.3e-09;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ORVEILGRTCVLSNLRGTRY 23  
Db 194 ORVEILGRTCVLSNLRGTRY 216

RESULT 15  
AAR47518 standard; protein; 508 AA.

XX AAR47518  
AC AAR47518  
XX  
XX 25-MAR-2003 (revised)  
DT 24-JUN-1994 (first entry)  
XX  
XX Human EPO receptor.  
DE  
XX  
XX Erythropoietin receptor; recombinant; murine; anaemia.  
KW

XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
XX FT Peptide 1..24  
XX FT /note= "signal peptide"  
XX FT Protein 25..508  
XX FT /note= "mature EPO receptor"  
XX FT Region 251..272  
XX FT /note= "putative transmembrane domain"  
XX  
XX US5278065-A.  
XX  
XX 11-JAN-1994.  
PD  
XX  
XX 25-MAR-1991; 91US-00678877.  
PF  
XX  
XX 03-FEB-1989; 89US-00306503.  
PR  
XX  
XX (GEM) GENETICS INST INC.  
PA (CHIL-) CHILDRENS MEDICAL CENT.  
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.  
XX  
XX D'andrea A, Wong GG, Jones SS;  
PI  
XX  
XX WPI; 1994-025409/03.  
DR  
DR N-PSDB; AAQ53995.  
XX  
XX Recombinant DNA encoding erythropoietin receptor - used to develop prods.  
PT for study, treatment or diagnosis of disorders in which receptor is  
PT dysfunctional.  
XX  
XX Disclosure; Fig 9; 24pp; English.  
PS  
XX  
XX Mouse erythroleukemia (MEL) cells were used to construct a cDNA library.  
CC The cDNA was used to transfect COS-1 cells and these were screened for  
CC radioiodinated erythropoietin (EPO) binding to isolate cDNA encoding the  
CC EPO receptor. This cDNA was used as a probe to screen a human genomic  
CC cDNA library to obtain DNA encoding the human EPO receptor. The cDNA may  
CC be used to study, treat or diagnose disorders in which the EPO receptor  
CC is dysfunctional. The EPO receptor may also be used to raise antibodies or  
CC for treating hypersensitivity to EPO or who have elevated levels of EPO.  
CC The prod. is pref. used for treating anaemias, primary proliferative  
CC polycythemia and secondary polycythemia. See also AAR47517. (Updated on  
CC 25-MAR-2003 to correct PF field.)  
XX  
XX Sequence 508 AA;

Query Match 100.0%; Score 117; DB 2; Length 508;  
Best Local Similarity 100.0%; Pred. No. 1.3e-09;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ORVEILGRTCVLSNLRGTRY 23  
Db 194 ORVEILGRTCVLSNLRGTRY 216

Search completed: May 6, 2004, 12:45:02  
Job time : 55 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: May 6, 2004, 12:42:22 ; Search time 23 Seconds  
(without alignments)  
51.626 Million cell updates/sec

Title: US-10-612-885A-1

Perfect score: 117

Sequence: 1 QRVLEIGRTECVLSNLRGRTRY 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	117	100.0	23	4	US-09-028-937-11
2	117	100.0	30	2	US-08-280-864A-12
3	117	100.0	30	4	US-09-092-291-12
4	117	100.0	438	4	US-09-339-838-5
5	117	100.0	438	4	US-09-339-838-7
6	117	100.0	488	3	US-08-776-511-2
7	117	100.0	508	2	US-08-850-293-5
8	49	41.9	321	3	US-09-039-609-4
9	49	41.9	458	3	US-09-039-609-2
10	46	39.3	64	4	US-09-134-000C-5287
11	46	39.3	67	4	US-09-732-210-1599
12	46	39.3	67	4	US-09-732-210-1500
13	45	38.5	372	4	US-09-252-991A-32067
14	44	37.6	493	4	US-09-489-039A-12903
15	43	36.8	931	4	US-08-624-655A-2
16	42	35.9	67	4	US-09-732-210-1601
17	42	35.9	252	4	US-09-252-991A-32222
18	42	35.9	283	4	US-08-956-171E-5203
19	42	35.9	363	4	US-09-134-000C-3764
20	42	35.9	605	2	US-08-752-307B-8
21	42	35.9	605	4	US-09-707-802-8
22	42	35.9	605	4	US-09-991-326-8
23	42	35.9	623	4	US-09-252-991A-23930
24	42	35.9	1018	1	US-08-452-052-2
25	42	35.9	1101	3	US-08-986-485-2
26	42	35.9	1611	2	US-08-804-227C-5
27	42	35.9	3729	2	US-08-804-227C-4

28	42	35.9	4472	2	US-08-804-227C-2	Sequence 2, Appli
29	42	35.9	4545	2	US-08-804-227C-14	Sequence 14, Appl
30	41	35.0	50	4	US-09-621-976-6212	Sequence 6212, Ap
31	41	35.0	60	4	US-08-754-477A-14	Sequence 14, Appl
32	41	35.0	60	4	US-08-754-477A-15	Sequence 15, Appl
33	41	35.0	75	3	US-08-928-383B-13	Sequence 13, Appl
34	41	35.0	292	4	US-09-711-164-438	Sequence 438, App
35	41	35.0	327	4	US-09-134-001C-3535	Sequence 3535, Ap
36	41	35.0	749	4	US-09-252-991A-17331	Sequence 17331, A
37	41	35.0	835	4	US-09-758-282B-155	Sequence 155, App
38	41	35.0	835	4	US-09-758-282B-243	Sequence 243, App
39	41	35.0	843	4	US-09-489-039A-7545	Sequence 7545, Ap
40	41	35.0	865	4	US-09-252-991A-20894	Sequence 20894, A
41	41	35.0	1018	1	US-08-408-093-6	Sequence 6, Appli
42	41	35.0	1018	1	US-08-408-420A-6	Sequence 6, Appli
43	41	35.0	1018	1	US-08-714-901-6	Sequence 6, Appli
44	41	35.0	1018	3	US-08-040-741-6	Sequence 6, Appli
45	41	35.0	1091	3	US-08-986-485-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1  
US-09-028-937-11  
; Sequence 11, Application US/09028937  
; Patent No 6333031  
; GENERAL INFORMATION:  
; APPLICANT: Olsson, Lennart  
; APPLICANT: Naranda, Tatjana  
; TITLE OF INVENTION: Receptor Derived Peptides As Modulators  
; TITLE OF INVENTION: Of Receptor Activity  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hombach, Test, Albritton & Herbert  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/09/028,937  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA: US 08/788,820  
; FILING DATE: 23-JAN-1997  
; PRIOR APPLICATION DATA: US 08/701,382  
; FILING DATE: 22-AUG-1996  
; APPLICATION NUMBER: US 08/612,999  
; FILING DATE: 08-MAR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Silva, Robin M.  
; REGISTRATION NUMBER: 38,304  
; REFERENCE/DOCKET NUMBER: A-63139-3/RFT/RMS  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 949-8711  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 23 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
US-09-028-937-11

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/092,291  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/280864  
FILING DATE: 25-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-307A  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-092-291-12

Query Match 100.0%; Score 117; DB 4; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.3e-12; Indels 0; Gaps 0;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRVLEGRTECVLSNLRGRTRY 23  
DB 1 QRVLEGRTECVLSNLRGRTRY 23

RESULT 2  
US-08-280-864A-12  
Sequence 12, Application US/08280864A  
Patent No. 585574  
GENERAL INFORMATION:  
APPLICANT: Eliott, Steven G.  
TITLE OF INVENTION: Antibodies Which Activate an Erythropoietin Receptor  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Behavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/280,864A  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-307  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-280-864A-12

Query Match 100.0%; Score 117; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.8e-12; Indels 0; Gaps 0;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRVLEGRTECVLSNLRGRTRY 23  
DB 1 QRVLEGRTECVLSNLRGRTRY 23

RESULT 3  
US-09-092-291-12  
Sequence 12, Application US/09092291  
Patent No. 6319499  
GENERAL INFORMATION:  
APPLICANT: Eliott, Steven G.  
TITLE OF INVENTION: Antibodies Which Activate an Erythropoietin Receptor  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: One Amgen Center Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 91320  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/092,291  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/280864  
FILING DATE: 25-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-307A  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-092-291-12

Query Match 100.0%; Score 117; DB 4; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.8e-12; Indels 0; Gaps 0;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRVLEGRTECVLSNLRGRTRY 23  
DB 1 QRVLEGRTECVLSNLRGRTRY 23

RESULT 4  
US-09-339-838-5  
Sequence 5, Application US/09339838  
Patent No. 6361998  
GENERAL INFORMATION:  
APPLICANT: Bell, David N.  
APPLICANT: Mueller, Susan G.  
APPLICANT: Matthews, Kathryn E.  
TITLE OF INVENTION: The Efficient Culture of Stem Cells for the Production of Hemoglobin  
CURRENT APPLICATION NUMBER: US/09/339,838  
FILING DATE: 1999-06-25  
PRIOR APPLICATION NUMBER: CA 2,260,332  
PRIOR FILING DATE: 1999-01-25  
PRIOR APPLICATION NUMBER: CA 2,241,576  
PRIOR FILING DATE: 1998-06-25  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 5  
LENGTH: 438  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-339-838-5

Query Match 100.0%; Score 117; DB 4; Length 438;  
Best Local Similarity 100.0%; Pred. No. 4.3e-11; Indels 0; Gaps 0;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRVLEGRTECVLSNLRGRTRY 23  
DB 194 QRVLEGRTECVLSNLRGRTRY 216

RESULT 5  
US-09-339-838-7  
Sequence 7, Application US/09339838  
Patent No. 6361998  
GENERAL INFORMATION:  
APPLICANT: Bell, David N.  
APPLICANT: Mueller, Susan G.  
APPLICANT: Matthews, Kathryn E.



;; TITLE OF INVENTION: The Efficient Culture of Stem Cells for the Production of Hemoglo  
;; FILE REFERENCE: 6704-83  
;; CURRENT APPLICATION NUMBER: US/09/339,838  
;; CURRENT FILING DATE: 1999-06-25  
;; PRIOR APPLICATION NUMBER: CA 2,260,332  
;; PRIOR FILING DATE: 1999-01-25  
;; PRIOR APPLICATION NUMBER: CA 2,241,576  
;; PRIOR FILING DATE: 1998-06-25  
;; NUMBER OF SEQ ID NOS: 11  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 7  
;; LENGTH: 438  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-339-838-7

Query Match 100.0%; Score 117; DB 4; Length 438;  
Best Local Similarity 100.0%; Pred. No. 4.3e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRVILEGRTECVLSNLRGRTRY 23  
Db 194 QRVILEGRTECVLSNLRGRTRY 216

RESULT 6  
US-08-776-511-2  
;; Sequence 2, Application US/08776511  
;; Patent No. 6153190  
;; GENERAL INFORMATION:  
;; APPLICANT: Young, Peter R.  
;; APPLICANT: Erickson-Miller, Connie  
;; TITLE OF INVENTION: Method for Obtaining Receptor Agonist  
;; TITLE OF INVENTION: Antibodies  
;; NUMBER OF SEQUENCES: 13  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: SmithKline Beecham Corporation- Corporate  
;; ADDRESSEE: Patents  
;; STREET: 709 Swedeland Road  
;; CITY: King of Prussia  
;; STATE: Pennsylvania  
;; COUNTRY: USA  
;; ZIP: 19406-2799  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/776,511  
;; FILING DATE:  
;; CLASSIFICATION: 424  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Jervis, Herbert H.  
;; REGISTRATION NUMBER: 31,171  
;; REFERENCE/DOCKET NUMBER: SEC P50349-1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 610-270-5015  
;; TELEFAX: 610-270-5030  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 488 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-776-511-2

Query Match 100.0%; Score 117; DB 3; Length 488;  
Best Local Similarity 100.0%; Pred. No. 4.9e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRVILEGRTECVLSNLRGRTRY 23  
Db 194 QRVILEGRTECVLSNLRGRTRY 216

RESULT 7  
US-08-850-293-5  
;; Sequence 5, Application US/08850293  
;; Patent No. 5843726  
;; GENERAL INFORMATION:  
;; APPLICANT: Lee, Jong Y.  
;; TITLE OF INVENTION: PURIFIED HUMAN ERYTHROPOIETIN RECEPTOR  
;; TITLE OF INVENTION: PROTEIN FRAGMENT AND ANTIBODIES DERIVED THEREFROM  
;; NUMBER OF SEQUENCES: 5  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Fish & Richardson P.C., P.A.  
;; STREET: 60 South Sixth Street, Suite 3300  
;; CITY: Minneapolis  
;; STATE: MN  
;; COUNTRY: USA  
;; ZIP: 55402  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM compatible  
;; OPERATING SYSTEM: DOS  
;; SOFTWARE: FastSeq for Windows Version 2.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/850,293  
;; FILING DATE: 05-MAY-1997  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/499,643  
;; FILING DATE: 07-JUL-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/106,815  
;; FILING DATE: 16-AUG-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Ellinger, Mark S.  
;; REGISTRATION NUMBER: 34,812  
;; REFERENCE/DOCKET NUMBER: 07004/002001  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 612/335-5070  
;; TELEFAX: 612/288-9696  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 508 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-850-293-5

Query Match 100.0%; Score 117; DB 2; Length 508;  
Best Local Similarity 100.0%; Pred. No. 5.2e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRVILEGRTECVLSNLRGRTRY 23  
Db 194 QRVILEGRTECVLSNLRGRTRY 216

RESULT 8  
US-09-039-609-4  
;; Sequence 4, Application US/09039609  
;; Patent No. 6107473  
;; GENERAL INFORMATION:  
;; APPLICANT: ALBONE, EARL  
;; APPLICANT: KIKLY, KRISTINE  
;; TITLE OF INVENTION: A KRINGLE-RELATED CLONE,  
;; TITLE OF INVENTION: HTHB247  
;; NUMBER OF SEQUENCES: 4  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Ratner & Prestia  
;; STREET: P.O. Box 980  
;; CITY: Valley Forge  
;; STATE: PA



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; TYPE: PRT
; ORGANISM: Kluyveromyces lactis
US-09-732-210-1599

Query Match
Best Local Similarity 39.3%; Score 46; DB 4; Length 67;
Matches 9; Conservative 4; Mismatches 8; Indels 8; Gaps 0;

Qy 2 RVEILGRTTCVLSNLRGRTR 22
Db 29 RVEFLDTRTIVRVKGPVR 49

RESULT 12
US-09-732-210-1600
; Sequence 1600, Application US/09732210
; Patent No. 8573361
; GENERAL INFORMATION:
; APPLICANT: Bunkers, Greg J.
; APPLICANT: Liang, Jihong
; APPLICANT: Mittanck, Cindy A.
; APPLICANT: Seale, Jeffrey W.
; APPLICANT: Wu, Yonnie S.
; TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
; FILE REFERENCE: 38-21(15036)B
; CURRENT APPLICATION NUMBER: US/09/732,210
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,513
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: US 60/169,340
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 1753
; SEQ ID NO 1500
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Kluyveromyces marxianus
US-09-732-210-1600

Query Match
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Matches 9; Conservative 4; Mismatches 8; Indels 8; Gaps 0;

Qy 2 RVEILGRTTCVLSNLRGRTR 22
Db 29 RVEFLDTRTIVRVKGPVR 49

RESULT 13
US-09-252-991A-32067
; Sequence 32067, Application US/09252991A
; Patent No. 5551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32067
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32067

Query Match
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Matches 12; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

Qy 2 RVEILGRTTCVLSNLRGRTR 23
Db 251 RVAVLGRVE--LSPLHGRGRW 270

RESULT 14
US-09-489-039A-12903
; Sequence 12903, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12903
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12903

Query Match
Best Local Similarity 37.6%; Score 44; DB 4; Length 493;
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 4 EILEGRTTCVLSNLRGRTR 23
Db 111 EALEGKTFCVRVRKRGKHEP 130

RESULT 15
US-08-624-655A-2
; Sequence 2, Application US/08624655A
; Patent No. 6323005
; GENERAL INFORMATION:
; APPLICANT: DABAN, MONTERRAT
; APPLICANT: MEDRANO, ANDRES
; APPLICANT: ESPUNA, ENRIC
; APPLICANT: QUEROL, ENRIQUE
; TITLE OF INVENTION: TRANSFERRIN-BINDING PROTEIN 1 (Tbpl) GENE OF
; TITLE OF INVENTION: Actinobacillus pleuropneumoniae, ITS USE TO PREPARE
; TITLE OF INVENTION: PRODUCTS FOR THE UTILIZATION IN VACCINES FOR
; TITLE OF INVENTION: PLEURO-PNEUMONIA AND AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: P00740
; CURRENT APPLICATION NUMBER: US/08/624,655A
; CURRENT FILING DATE: 1996-03-22
; PRIOR APPLICATION NUMBER: 95 00592
; PRIOR FILING DATE: 1995-03-24
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 931
; TYPE: PRT
; ORGANISM: Actinobacillus pleuropneumoniae
US-08-624-655A-2

Query Match
Best Local Similarity 36.8%; Score 43; DB 4; Length 931;
Matches 6; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 6 LEGRTECVLSNLRGRTR 23
Db 581 IAGRADCATSKIRGHNY 598

Search completed: May 6, 2004, 12:46:53
Job time : 23 secs
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GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: May 6, 2004, 12:45:07 ; Search time 42 Seconds  
(without alignments)  
152.001 Million cell updates/sec

Title: US-10-612-885A-1

Perfect score: 117

Sequence: 1 QRVLEIGRTECVLSNLRGTRY 23

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Gapop 10.0 , Gapext 0.5

Searched: 1140673 seqs, 277566755 residues

Total number of hits satisfying chosen parameters: 1140673

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Published Applications AA:\*

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- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
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- 11: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
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- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	117	100.0	23	9	US-09-991-548-11
2	117	100.0	23	16	US-10-231-494-30
3	117	100.0	30	15	US-10-364-276-12
4	117	100.0	458	12	US-10-287-971-48
5	117	100.0	458	12	US-10-287-971-50
6	117	100.0	458	12	US-10-287-971-52
7	117	100.0	508	9	US-09-016-159-5
8	115	96.6	508	12	US-10-287-971-54
9	105	88.0	109	15	US-10-316-194-142
10	95	82.1	109	15	US-10-316-194-144
11	93	79.5	109	15	US-10-316-194-35
12	86	73.5	109	15	US-10-316-194-43
13	52	44.4	1026	10	US-09-947-063-4
14	52	44.4	1026	10	US-09-947-063-11
15	45	41.9	49	9	US-09-728-912-7

16	49	41.9	110	14	US-10-029-386-27439	Sequence 27439, A
17	49	41.9	341	9	US-09-848-288-4	Sequence 4, Appli
18	49	41.9	373	10	US-09-759-1308-376	Sequence 376, App
19	49	41.9	373	13	US-10-042-431-6	Sequence 6, Appli
20	49	41.9	413	9	US-09-728-912-2	Sequence 2, Appli
21	49	41.9	451	10	US-09-759-1308-413	Sequence 413, App
22	49	41.9	451	13	US-10-042-431-43	Sequence 43, Appl
23	49	41.9	456	10	US-09-759-1308-375	Sequence 375, App
24	49	41.9	456	13	US-10-042-431-5	Sequence 5, Appli
25	49	41.9	458	16	US-10-467-042-16	Sequence 16, Appl
26	49	41.9	470	10	US-09-759-1308-439	Sequence 439, App
27	49	41.9	470	13	US-10-042-431-69	Sequence 69, Appl
28	49	41.9	475	10	US-09-759-1308-373	Sequence 373, App
29	49	41.9	475	13	US-10-042-431-3	Sequence 3, Appli
30	49	41.9	492	15	US-10-094-749-2546	Sequence 2546, Ap
31	48	41.0	312	9	US-09-738-626-5282	Sequence 5282, Ap
32	47.5	40.6	419	15	US-10-369-493-9725	Sequence 9725, Ap
33	47	40.2	85	14	US-10-029-386-32900	Sequence 32900, A
34	47	40.2	191	12	US-10-424-599-181458	Sequence 181458,
35	47	40.2	386	12	US-10-424-599-181457	Sequence 181457,
36	46	39.3	494	12	US-10-425-114-50005	Sequence 50005, A
37	46	39.3	941	12	US-10-425-114-72012	Sequence 72012, A
38	45	38.5	686	15	US-10-162-335-46	Sequence 46, Appl
39	45	38.5	686	15	US-10-162-335-48	Sequence 48, Appl
40	45	38.5	686	15	US-10-162-335-50	Sequence 50, Appl
41	45	38.5	686	15	US-10-162-335-52	Sequence 52, Appl
42	45	38.5	961	15	US-10-162-335-42	Sequence 42, Appl
43	44	37.6	87	12	US-10-424-599-196538	Sequence 196538,
44	44	37.6	250	12	US-10-424-599-236053	Sequence 236053,
45	44	37.6	873	12	US-10-425-114-65968	Sequence 65968, A

## ALIGNMENTS

### RESULT 1

US-09-991-548-11  
; Sequence 11, Application US/09991548.  
; Patent No. US20020160013A1  
; GENERAL INFORMATION:  
; APPLICANT: OLSSON, Lennart  
; APPLICANT: NARANDA, Tatjana  
; TITLE OF INVENTION: RECEPTOR DERIVED PEPTIDES AS MODULATORS  
; TITLE OF INVENTION: OF RECEPTOR ACTIVITY  
; FILE REFERENCE: 213542000101  
; CURRENT APPLICATION NUMBER: US/09/991,548  
; CURRENT FILING DATE: 2001-11-20  
; PRIOR APPLICATION NUMBER: 09/028,937  
; PRIOR FILING DATE: 1998-02-24  
; PRIOR APPLICATION NUMBER: 08/788,820  
; PRIOR FILING DATE: 1997-01-23  
; PRIOR APPLICATION NUMBER: 08/701,382  
; PRIOR FILING DATE: 1996-08-22  
; PRIOR APPLICATION NUMBER: 08/612,999  
; PRIOR FILING DATE: 1996-03-08  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 23  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: human erythropoietin receptor  
US-09-991-548-11

Query Match 100.0%; Score 117; DB 9; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRVLEIGRTECVLSNLRGTRY 23

Db 1 QRVLEIGRTECVLSNLRGTRY 23

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RESULT 2
US-10-231-494-30
; Sequence 30, Application US/10231494
; Publication No. US2004002334A1
; GENERAL INFORMATION:
; APPLICANT: Prior, Christopher P.
; TITLE OF INVENTION: Modified Transferrin Fusion Proteins
; FILE REFERENCE: 54710-5001-US
; CURRENT APPLICATION NUMBER: US/10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: EPO mimetic
US-10-231-494-30

Query Match      100.0%; Score 117; DB 16; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.8e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRVLEIGRTECVLSNLGRTRY 23
Db 1 QRVLEIGRTECVLSNLGRTRY 23

RESULT 3
US-10-364-276-12
; Sequence 12, Application US/10364276
; Publication No. US2003021544A1
; GENERAL INFORMATION:
; APPLICANT: Eliott, Steven G
; TITLE OF INVENTION: Antibodies which Activate an Erythropoietin Receptor
; FILE REFERENCE: 06843-0030-0400
; CURRENT APPLICATION NUMBER: US/10/364,276
; PRIOR FILING DATE: 2003-06-17
; PRIOR APPLICATION NUMBER: 09/092,671
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 08/280,864
; PRIOR FILING DATE: 1994-07-26
; PRIOR APPLICATION NUMBER: 09/640,090
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-364-276-12

Query Match      100.0%; Score 117; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRVLEIGRTECVLSNLGRTRY 23
Db 1 QRVLEIGRTECVLSNLGRTRY 23

RESULT 4
US-10-287-971-48
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; Sequence 48, Application US/10287971
; Publication No. US20040067882A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-480A
; CURRENT APPLICATION NUMBER: US/10/287,971
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 09/997,425
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 10/035,568
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/338,626
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/401,479
; PRIOR FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/333,072
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 60/348,283
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/393,262
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: 60/406,181
; PRIOR FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 397
; SOFTWARE: Curaseq1ist version 0.1
; SEQ ID NO 48
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-971-48

Query Match      100.0%; Score 117; DB 12; Length 458;
Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRVLEIGRTECVLSNLGRTRY 23
Db 194 QRVLEIGRTECVLSNLGRTRY 216

RESULT 5
US-10-287-971-50
; Sequence 50, Application US/10287971
; Publication No. US20040067882A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-480A
; CURRENT APPLICATION NUMBER: US/10/287,971
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 09/997,425
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 10/035,568
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/338,626
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/401,479
; PRIOR FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/333,072
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 60/348,283
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/393,262
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: 60/406,181
; PRIOR FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 397
; SOFTWARE: Curaseq1ist version 0.1
; SEQ ID NO 50
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-287-971-50
Query Match      100.0%; Score 117; DB 12; Length 458;
Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRVLEGRTECVLSNLRGRTRY 23
Db 194 QRVLEGRTECVLSNLRGRTRY 216

RESULT 6
US-10-287-971-52
Sequence 52, Application US/10287971
Publication No. US20040067882A1
GENERAL INFORMATION:
APPLICANT: Alsbrook, et al
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-480A
CURRENT APPLICATION NUMBER: US/10/287,971
CURRENT FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 09/997,425
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: 10/035,568
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: 60/338,626
PRIOR FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: 60/401,479
PRIOR FILING DATE: 2002-08-06
PRIOR APPLICATION NUMBER: 60/333,072
PRIOR FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: 60/348,283
PRIOR FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: 60/393,262
PRIOR FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: 60/406,181
PRIOR FILING DATE: 2002-08-26
SOFTWARE: Curasequest version 0.1
SEQ ID NO 52
LENGTH: 458
TYPE: PRT
ORGANISM: Homo sapiens
US-10-287-971-52

Query Match      100.0%; Score 117; DB 12; Length 458;
Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRVLEGRTECVLSNLRGRTRY 23
Db 194 QRVLEGRTECVLSNLRGRTRY 216

RESULT 7
US-09-016-159-5
Sequence 5, Application US/09016159
Patent No. US20020031806A1
GENERAL INFORMATION:
APPLICANT: Lee, Jong Y.
TITLE OF INVENTION: PURIFIED HUMAN ERYTHROPOIETIN RECEPTOR
TITLE OF INVENTION: PROTEIN FRAGMENT AND ANTIBODIES DERIVED THEREFROM
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: Fish & Richardson P.C., P.A.
STREET: 60 South Sixth Street, Suite 3300
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM compatible

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OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,159
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/876,227
FILING DATE: 16-JUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/734,097
FILING DATE: 21-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/460,525
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ellinger, Mark S.
REGISTRATION NUMBER: 34,812
REFERENCE/DOCKET NUMBER: 07004/002003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/335-5070
TELEFAX: 612/288-9696
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 508 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-159-5

Query Match      100.0%; Score 117; DB 9; Length 508;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRVLEGRTECVLSNLRGRTRY 23
Db 194 QRVLEGRTECVLSNLRGRTRY 216

RESULT 8
US-10-287-971-54
Sequence 54, Application US/10287971
Publication No. US20040067882A1
GENERAL INFORMATION:
APPLICANT: Alsbrook, et al
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METIC
FILE REFERENCE: 21402-480A
CURRENT APPLICATION NUMBER: US/10/287,971
CURRENT FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 09/997,425
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: 10/035,568
PRIOR FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 60/338,626
PRIOR FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: 60/401,479
PRIOR FILING DATE: 2002-08-06
PRIOR APPLICATION NUMBER: 60/333,072
PRIOR FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: 60/348,283
PRIOR FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: 60/393,262
PRIOR FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: 60/406,181
PRIOR FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 397
SOFTWARE: Curasequest version 0.1
SEQ ID NO 54
LENGTH: 508
TYPE: PRT
ORGANISM: Homo sapiens
US-10-287-971-54

Query Match      96.6%; Score 113; DB 12; Length 508;

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Best Local Similarity 95.7%; Pred. NO. 2.7e-09;  
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QRVLEGRTECVLSNLRGRTRY 23  
Db 194 QRVKLEGRTECVLSNLRGRTRY 216

RESULT 9  
US-10-316-194-142  
; Sequence 142, Application US/10316194  
; Publication No. US20030215914A1  
; GENERAL INFORMATION:  
; APPLICANT: Houtzager, Erwin  
; APPLICANT: Vijjn, Irma M.C.  
; APPLICANT: Sijmons, Peter C.  
; TITLE OF INVENTION: A structure for presenting desired peptide sequences  
; FILE REFERENCE: 2183-5610US  
; CURRENT APPLICATION NUMBER: US/10/316,194  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: US 10/016,516  
; PRIOR FILING DATE: 2001-12-10  
; NUMBER OF SEQ ID NOS: 173  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 142  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: IMABIS020  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1)..(109)  
US-10-316-194-142

Query Match 88.0%; Score 103; DB 15; Length 109;  
Best Local Similarity 91.3%; Pred. No. 1.8e-08;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 QRVLEGRTECVLSNLRGRTRY 23  
Db 46 QRVBNMGRTECVLSNLRGRTRY 68

RESULT 10  
US-10-316-194-144  
; Sequence 144, Application US/10316194  
; Publication No. US20030215914A1  
; GENERAL INFORMATION:  
; APPLICANT: Houtzager, Erwin  
; APPLICANT: Vijjn, Irma M.C.  
; APPLICANT: Sijmons, Peter C.  
; TITLE OF INVENTION: A structure for presenting desired peptide sequences  
; FILE REFERENCE: 2183-5610US  
; CURRENT APPLICATION NUMBER: US/10/316,194  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: US 10/016,516  
; PRIOR FILING DATE: 2001-12-10  
; NUMBER OF SEQ ID NOS: 173  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 144  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: IMABIS027  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1)..(109)  
US-10-316-194-144

Query Match 82.1%; Score 96; DB 15; Length 109;  
Best Local Similarity 87.0%; Pred. No. 2.3e-07;

Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 QRVLEGRTECVLSNLRGRTRY 23  
Db 46 QRVBNMGRTECVLSNLRGRTRY 68

RESULT 11  
US-10-316-194-35  
; Sequence 35, Application US/10316194  
; Publication No. US20030215914A1  
; GENERAL INFORMATION:  
; APPLICANT: Houtzager, Erwin  
; APPLICANT: Vijjn, Irma M.C.  
; APPLICANT: Sijmons, Peter C.  
; TITLE OF INVENTION: A structure for presenting desired peptide sequences  
; FILE REFERENCE: 2183-5610US  
; CURRENT APPLICATION NUMBER: US/10/316,194  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: US 10/016,516  
; PRIOR FILING DATE: 2001-12-10  
; NUMBER OF SEQ ID NOS: 173  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 35  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: VAP amino acid  
; OTHER INFORMATION: sequence of iMab600  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1)..(109)  
US-10-316-194-35

Query Match 79.5%; Score 93; DB 15; Length 109;  
Best Local Similarity 87.0%; Pred. No. 6.7e-07;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 QRVLEGRTECVLSNLRGRTRY 23  
Db 46 QRVBNMGRTECVLSNLRGRTRY 68

RESULT 12  
US-10-316-194-43  
; Sequence 43, Application US/10316194  
; Publication No. US20030215914A1  
; GENERAL INFORMATION:  
; APPLICANT: Houtzager, Erwin  
; APPLICANT: Vijjn, Irma M.C.  
; APPLICANT: Sijmons, Peter C.  
; TITLE OF INVENTION: A structure for presenting desired peptide sequences  
; FILE REFERENCE: 2183-5610US  
; CURRENT APPLICATION NUMBER: US/10/316,194  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: US 10/016,516  
; PRIOR FILING DATE: 2001-12-10  
; NUMBER OF SEQ ID NOS: 173  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 43  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: VAP amino acid  
; OTHER INFORMATION: sequence of iMab1100  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1)..(109)  
US-10-316-194-43

Query Match 73.5%; Score 86; DB 15; Length 109;



Best Local Similarity 82.6%; Pred. No. 8.6e-06;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 ORVEILGRTECVLSNLRGRTRY 23  
Db 46 ORVEILNMGTSVLSNLRGRTRY 68  
RESULT 13  
US-09-947-063-4  
; Sequence 4, Application US/09947063  
; Publication No. US20030059775A1  
; GENERAL INFORMATION:  
; APPLICANT: Padigaru et al.  
; TITLE OF INVENTION: No. US20030059775A1el Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-112  
; CURRENT APPLICATION NUMBER: US/09/947,063  
; CURRENT FILING DATE: 2001-09-05  
; PRIOR APPLICATION NUMBER: 60/229,990  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 60/229,988  
; PRIOR FILING DATE: 2000-09-05  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 1026  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-947-063-4  
Query Match 44.4%; Score 52; DB 10; Length 1026;  
Best Local Similarity 71.4%; Pred. No. 27;  
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
Qy 7 EGRTECVLSNLRGR 20  
Db 292 EGFYECIASNLRGR 305  
RESULT 14  
US-09-947-063-11  
; Sequence 11, Application US/09947063  
; Publication No. US20030059775A1  
; GENERAL INFORMATION:  
; APPLICANT: Padigaru et al.  
; TITLE OF INVENTION: No. US20030059775A1el Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-112  
; CURRENT APPLICATION NUMBER: US/09/947,063  
; CURRENT FILING DATE: 2001-09-05  
; PRIOR APPLICATION NUMBER: 60/229,990  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 60/229,988  
; PRIOR FILING DATE: 2000-09-05  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 1026  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-947-063-11  
Query Match 44.4%; Score 52; DB 10; Length 1026;  
Best Local Similarity 71.4%; Pred. No. 27;  
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
Qy 7 EGRTECVLSNLRGR 20  
Db 292 EGFYECIASNLRGR 305  
RESULT 15  
US-09-728-912-7  
; Sequence 7, Application US/09728912

Patent No. US20010036643A1  
; GENERAL INFORMATION:  
; APPLICANT: Holloway, James L.  
; TITLE OF INVENTION: Tumor Necrosis Factor-Stimulated Gene  
; TITLE OF INVENTION: and Protein  
; FILE REFERENCE: 99-94US  
; CURRENT APPLICATION NUMBER: US/09/728,912  
; CURRENT FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: 60/169,252  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 7  
; LENGTH: 49  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-728-912-7  
Query Match 41.9%; Score 49; DB 9; Length 49;  
Best Local Similarity 50.0%; Pred. No. 2.4;  
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
Qy 3 VEILEGRTECVLSNLRGRTR 22  
Db 7 VELLGTYTHRYLARFHGRSR 26  
Search completed: May 6, 2004, 12:48:22  
Job time : 43 secs

Best Local Similarity 82.6%; Pred. No. 8.6e-06;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 ORVEILGRTECVLSNLRGRTRY 23  
Db 46 ORVEILNMGTSVLSNLRGRTRY 68  
RESULT 13  
US-09-947-063-4  
; Sequence 4, Application US/09947063  
; Publication No. US20030059775A1  
; GENERAL INFORMATION:  
; APPLICANT: Padigaru et al.  
; TITLE OF INVENTION: No. US20030059775A1el Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-112  
; CURRENT APPLICATION NUMBER: US/09/947,063  
; CURRENT FILING DATE: 2001-09-05  
; PRIOR APPLICATION NUMBER: 60/229,990  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 60/229,988  
; PRIOR FILING DATE: 2000-09-05  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 1026  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-947-063-4  
Query Match 44.4%; Score 52; DB 10; Length 1026;  
Best Local Similarity 71.4%; Pred. No. 27;  
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
Qy 7 EGRTECVLSNLRGR 20  
Db 292 EGFYECIASNLRGR 305  
RESULT 14  
US-09-947-063-11  
; Sequence 11, Application US/09947063  
; Publication No. US20030059775A1  
; GENERAL INFORMATION:  
; APPLICANT: Padigaru et al.  
; TITLE OF INVENTION: No. US20030059775A1el Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-112  
; CURRENT APPLICATION NUMBER: US/09/947,063  
; CURRENT FILING DATE: 2001-09-05  
; PRIOR APPLICATION NUMBER: 60/229,990  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 60/229,988  
; PRIOR FILING DATE: 2000-09-05  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 1026  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-947-063-11  
Query Match 44.4%; Score 52; DB 10; Length 1026;  
Best Local Similarity 71.4%; Pred. No. 27;  
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
Qy 7 EGRTECVLSNLRGR 20  
Db 292 EGFYECIASNLRGR 305  
RESULT 15  
US-09-728-912-7  
; Sequence 7, Application US/09728912

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